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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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1677
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10782.626 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AUTHORS	SOURCE	ACCESSION VERSION	RESULT 1 AX509034 LOCUS DEFINITION		Ω (4)	4.4	44	,00	ມແ	70	יט עכ	1 42 6	32	ი ი 31	φο	27	თ თ	.4.	221	- 0	C 198	70	15	(12 13	, <u>, ,</u> ,	Oνc		മ		ω.		Result No. S
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patent: WO 0216655-A 3729 28-FEB-2002;
The Scripps Research Institute (US) ; {
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Similarity 100.0%;
77; Conservative 0;
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                                                        CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACCGTCG
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_292 c 335 g 542 t
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DEFINITION 1
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AUTHORS
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VERSION
KEYWORDS
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AC003680 91854 bp Arabidopsis thaliana chromosome complete sequence. AC003680 AC003680.3 GI:20197048 N DNA BAC F17K2 linear 2 genomic sequence; PLN 11-MAR-2002

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Butaryota; Viridiplantae; Streptophyta; Embryophyta, Tracheophyta,
Spermarophyta; Vagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 9.854)
Lin, X., Kaul, S. Town, C.D., Benito, M.-I., Creasy, T.H., Haas, B.U.,
Mu,D., Maiti,R., Romning, C.M., Xoo, H., Fujii, C.Y., Utterback, T.R.,
Barnstead, M.E., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.

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gene
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VSDEKSTSSCSTDTTITDTALRGEDDDBEYLSLFSPGV"
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101n(57. 242,335. 747)
101n(57. 242,3480"
101ne="At2g45480"
100te="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="overlap with BAC clone F4L23 (AC002387:1. .1281)."
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profile (PDOC00100)"
                                                                                                     Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91854)
Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                     9712
                                                                                                                                                                                                                                                                                                                                                                                                                           BAC clone F17K2 is from Arabidopsis thaliana chromosome 2 and is near the molecular marker(s) FLS.
The orientation of the sequence is from SP6 to T7 end of the BAC
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                                                                                                                                                                                                                      Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdrown@rigr.org
On Apr 18, 2002 this sequence version replaced gi:6598396.
Address all correspondence to:at@rigr.org
Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence
Unpublished
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/mol type="genomic DNA"
/cultivar="Columbia"
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oin(<57. .242,335. .>747)
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/gene="At2g45490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1. .1281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="At2g45480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="CIC02E07"
/clone="F17K2"
                                                        (bases 1 to 91854)
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                                                                                      in, X
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                                                                                                                                                                                                                                                                                                                                          OMMENT
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// note="8ynonym: F17K2.3; predicted by genscan" complement (join (<2414. 3616,3639. 3825,3916. 3965, 4092. 4215,4582. 4712,4769. 4864,4948. 5188,5352. 5374,5506. 5585,5670. >5980))

// gene="AL2645500" complement (join (3414. 3616,3639. 3825,3916. 3965,4092. 4215,4582. 4712,4769. 4864,4948. 5188,5352. 5374,69ne="AL2645500" complement (join (3414. 3616,3639. 3825,3916. 3965,7990)]

// gene="AL2645500" complement (join (2414. 3616,3639. 1864,4948. 5188,5352. 5374,79ne="AL2645500" complement (join (2414. 3616,3639. 1864,4948. 5188,5352. ) codon_start=1
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GHSSRENMADLLGHGIFAUDGEKRRQQRKLSSFERSTRVLAEDFSCGVFRRNASKLVGF
VSFRALSGKAPDAQDLLARCTLDSIFKVGFQVELKCLDGFSKEGGEFMEAPDEGUVAT
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SRFILDFLWALKWFFRIGSGSKLKKSIATIDKFVYSLITTKRKELAKEQNTVVREDIL
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SRFILDFLWALKWFFRIGSGSKLKKSIATIDKFVYSLITTRKKELAKEQNTVVVENEDIL
SRFILDFRWANSKGDNIYYLAXAMGRAFFYNGABRYVENENDV
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IADFGWSVQSSNKRKTMCGTLDYLAPEMYENRDHDYAVDNYTIGILCYEFLYGNPPFR
AESQKDTFKRILKIDLSFPLTPNVSEEAKNLISQLLVKDPSKRLSIEKIMQHPWIVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEKEKVRSYREKISUMONOVSERLOALGVCMSENKRTVAYPSSASVSSTASRYRKTU
SOKTPVARGGVATPRNPKDAAASPKPVKESGNVYDDKLVEMINTTIVDRSPSVKMDDV
AGINGAKOALLEMVILPAKRRDLFTGIRRPARVTSLLGLLLFGPFGNGKTMLAKAVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESOATFFWSASSIJSKWIDSIMSTRSTSRNBASRRLKSEFIJQFDGYTSNPDDLVII
IGAINKPORLDDAVLRLVKRIYVPLPDSNVRKLLFRTKKKKCQPHSLSDGDIDKIVKE
TEGKLYRLCIKKKRPFISQVTDKRYSGSDLQALCEBAAMPIRELGANILTIQANKVLN
FSYSQINVBVCLSLKGLINRCYHVTGKISTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSFLRGIIDSFSSILNEESKKDPSVSSSSTSSESMNGIDGVPVT
NERIAYKLKGYFDLAKEEIAKGVRAEEWGLHDDALLHYRNAQRIMNEATSTPSPSYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8412, .9632)
/gene="At2g45520"
/note="synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6429. .8288
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8100. .>8288)
/gene="At2g45510"
8100. .8288)
9100. .8288)
/gene="At2g45510"
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/genne="At2g45520"
complement(join(8553..8678,8768..8903,8987..9120,9289..956,9459.")
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1655. .1750,1886. .2128,2260. .2388))
/cate="At2g45490"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="hypothetical protein"
protein_id="AAC06152.1"
db_xref="G1:2979543"
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/gene="At2g45500"
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9948...10670
/gene="At2g45530"
/gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITITCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTTGTTA 76689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAACTCGGAATCCAAAAACTCAAATTTACCAAATCAGCCCAAATTATTGATGATGCTGGCG 76449
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YERBSPHDSTRQVPEKKKRRRRNOWTDIRFEN
YERSPENDSTRQVPEKKKRRRRNOWTDIRFEN
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/rpt_family="(CA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAATGAATGGTATGCTGGCAAAAGTTGGTGGCTGCGAAAATTACAACATTATTGTTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTGGTGAAAGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAATGAATGGTATGCTGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATTATC 420
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/note="synonym: F17X2.6; supported by full length cDNA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nent (join(<10833...11272,11438...11560,11636...1237...1237...13033...13119,13244...13464...13548...13548...13546...13548...13548...13548...13548...13548...14419...1476...14730...14813.14926...14995,15396...15338...1624...16322...16455...16545...10733...17337...17431...17649...19748...19748...19746.18015...1865...18944...19734...19744...19746.18015...18613.18944...19734...19734...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748...19748..
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Pred. No. 0;
; Mismatches
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/rpt family="(CAG)n"
complement(10833. .25573)
/gene="At2g45540"
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complement (join(<10833. .
12454. .12937,13023. .131
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д	28 AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTA	Ψ
λq	541 GGAPCCGITIGITAGITAAICICAAGGCCACGITAICGCCAAIAITIGATI	TTTGAGTG 600 TTGAGTG 76209
A . Q	601 GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCCTCAACAATGTGG 	AACTGAAG 660. AACTGAAG 76149
ף א	661 AGAGTAGGGTCCAGGCCCACATTCACATTTTCGTTTTGTAGCCTTTC	
y b	721 FGCTTACGGTCCCTCTTCTGGTCGGTCGTATGTACAAGTAGCATAGCTAGGT 	3GTTCAAA 780 3GTTCAAA 76029
۵ ۸	781 CCCGAAACAAGTACCAACGAATCAAAATAAGTITGAATCGGTIACATCTAGI	FACCGTCG 840. FACCGTCG 75969
و لا	841 AACTTACAATCATATCGATACTATGGATTCTAGATACTAGTTGTATGT 	
> Q	901 CCGGATIGTACAAGTACACAAGTACATAAGTAIGCGTATATGTGACGG [
.	961 AAAGGACGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAC 	SACACTA 1 SACACTA 7
> 0	1021 ATTAGCTTTTTGGTGGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGT.	AAGTATG 1080 AAGTATG 75729
ە بد	1081 GGCTTACAGCTTTTTCCATAAARTTAAAGTAAATCTTTTTTTGCCTAACCAA 75728 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAA	AAAATT 1140 75669
. 0	1141 ATTGARATCTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAAT 	TTTGTAC 1200" TTTGTAC 75609
> 0	201 A 608 A	
	261. TICTGATITITGGAITITIGAAGCTITICTTAGGTTAAAAAAAAGAAGTATATTA	N
0 =5	CTGATTTTGGARTTTTGAAGCTTTTCTTAGGTTAAAAAGAAGAAGTATTTAG AAGAAAAACATTTTGTGAAAAGAGAAATAAGTTTACTGGACCCCATTGT	AAACAAT 75489 CAGATGG 1380
a	488 AAAAGAAAAACATTTTGTGAAAAGAGAAATAAAG	 CAGATGG 75429
> 0	1381 TCCCATAATAATACTGATAGAAGATAGAGCAATGGAAAGGAATTTGTTCACG [CGTGGTACAA 1440 CGTGGTACAA 75369
	1441 TCGGATGGTTCTTTAAAGCTCATCGAACACACATCAGGACCGTTGATTTTTCC 75368 TCGCAATCATCAACAACAACAACAGGACCGTTGATTTTTCC	GCATCAA 1500
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Mus musculus chromosome 16 clone RP23-1J12, WORKING DRAFT SEQUENCE, ACCEPT A unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 WWRHWINNITDTRYYWWWKRWARBITTVYDSMCNAKGMWRGMNWRAMKOWWAANNDAGAM 463
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Sciurognathi, Muridae, Murinae, Mus.
                        TCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATATCCGGATTGTACAAG
                                                                                           975 AGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTAATTAGCTTTTTGGT
                                                                                                                                                                                     882 HTRICKRIKYNNININARIVYWYHHAARRWMNAWWIRININININININACRUTRIWABW
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                                                                                                                  1035 GGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCCAAGTATGGGCTTACAGCTTTT
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DOB Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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KEYWORDS
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TITLE
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TRELGHKSDGETIRWLLENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTTNADSDMGE
NLMKKKRKRPSNSEYIDISDAVSASSGLAPIATTTTIQPPQALASSTVAQQLLPPQGMY
                                                                                                                                                                                                                                                                                                                                                                                                                  PMWALPSNAMIPTVGAFFLIPQIAGPSNQPQLLAFPAAAASPSSYVAAVQQASTWARP
BYLQVVPSSGFVSVSDVSGSNLSRATSVWAPSSSSGVTTGSSSSIATTTTHTLRDFSL
BYLGVCELHQFMSTTTARSSNH"
1174. . 1660
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                                                                                                                                                                                                                                                                                    'product="putative PCF2 DNA binding protein"
'protein id="AAL07063.1"
'db xref="GI:15810351"
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/mol type="genomic DNA"
/mol type="genomic DNA"
/ Lab_xref="taxon:32630"
/ Lab 141
/ note="consensus sequence of A.t., L.a.,
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                                                                    /clone="RAFL07-08-P04 (R10678)"
/note="This clone is in a modified pB (FLC-1) as a BamH1/XhoI insert.
ecctype: Columbia"
1.1660
1.102
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3.6%; Score 59.8; DB 6;
Best Local Similarity 10.5%; Pred. No. 0.031;
Matches 85; Conservative 299; Mismatches 422;
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Sequence 22 from Patent WO0111061.
AX083744
organism="Arabidopsis
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evidence=experimental
                 mol_type="mRNA"
db_xref="taxon:3702"
chromosome="2"
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Consensus quality: 197223 bases at least Q30
Consensus quality: 197223 bases at least Q30
Consensus quality: 197223 bases at least Q30
Consensus quality: 214345 bases at least Q30
Consensus quality: 214345 bases at least Q30
Estimated insert size: 257300; agarose-fp estimation
Quality coverage: 3.01 in Q20 bases; agarose-fp estimation
Quality coverage: 3.01 in Q20 bases; agarose-fp estimation

* NOTE: This is a "working draft' sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                2 (bases 1 to 300695)
DOB Joint Genome Institute.
Direct Submission
Submitted (01-SEP-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center: Code: JGI
Web site: http://www.jgi.doe.gov
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                                                                                                                                      Submitted (UN-FEB-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019° USA 3 (bases) Loo 94348) 3 (bases) Loo 94348) 3 (bases) Loo 94348) 3 (bases) Loo 94348) 4 (bases) Direct Submission Submission Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019 USA
                                                                                                                                                                                                                                                                                                     Kupfer,D., So,S., Wang,H. and Roe,B.A.
Direct Submission
Submitted (06-NOV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (19-NOV-2002) Department Of Chemistry, And Blochemistry,
The University Of Oklahoma, 620-Parrington Oval, Room 208, Norman,
OK 73019, USA
On Nov 6, 2002 this sequence version replaced gi:24462347.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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The University of Oklahoma
Center code: UOKNOR
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/clone="busml:7955"
/clone lib="Zebrafish PAC library"
/ 17974 c 16523 g 29348 t
                                     Kupfer,D., So,S., Wang, H. and Roe, B.A.
Danic rerio PAC Clone Dusm1-183133
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5 (bases 1 to 94348)
Kupfer, So,S., Wang,H. and Roe,B.A.
Direct Submission
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(bases 1 to 94348)
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/strain="AB"
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Danio rerio
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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6: gap of unknown length
7: contig of 23827 bp in
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of 15079 bp in length
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/organism="Mus musculus"
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Danio rerio clone busm1-183j13 ¢
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AC109580.14 GI:24635954
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Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T., Sato,S. and Tabata,S. Structural Analysis of a Lotus japonicus Genome. I. Sequence Features and Mapping of Sixty-six TAC clones which cover the 6.7 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLN 19-JUL-2002
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                                                                                                                                                                                                                                       APUU4952
Lotus japonicus genomic DNA, chromosome 1, clone:LjT19C08, TM0125, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-MAR-2002) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:Yn@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
                          1332 ATTTTGTGAAAAGAGAATAAAGTTTACTGGACCCCCATTGTACAGATGGTCCCATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                 Lotus japonicus
Bukaryota, Varidiplantae, Streptophyta, Embryophyta, Tracheoph
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosida I, Fabales, Fabaceae, Papilionoideae, Loteae,
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3.2%; Score 53.4; DB 8;
Best Local Similarity 45.6%; Pred. No. 0.34;
Matches 224; Conservative 0; Mismatches 266;
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/mol type="genomic DNA"
/db_xref="taxon:34305"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="LjT19C08"
/clone_lib="LjT library"
/note="TAC clone:TM0125"
17797 c 17022 g 27069
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AP004952.1 GI:21907970
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2 (bases 1 to 89551)
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                                                                                                   MPUIS676 1058 bp DNA linear INV 09-FBB-1996 Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial
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ILMFPLYBESDDNPLPANPLYTPIHQDEWYPLFAYSILRSIPNKLGGVIALPSSIC
ILVFLPMLNSNANSSTYPHSGLIMLFPMFMILTWLGSQVIEHPYIIMAGFFSMLY
FFNFILLKFSYKMDYFIYNKPFNN"
                                                                                                                                                                                                                                                                                                                                                                           Mitochondrial-DNA sequence evidence on the phylogeny of Australian jack-jumper ants of the Myrmecia pilosula complex Mol. Phylogenet. Evol. 4 (1), 20-30 (1995) 95346030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="FWGATVITNLVSTIPFLGSDITQWLWGGYSVSNATLSRFYSIHF
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Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata,
Pormicidae, Myrmecilnae, Myrmecilni, Myrmecia,
1 (bases 1 to 1058)
Crozier, R. H., Dobric, N., Imai, H. T., Graur, D., Cornuet, J. M.
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                                                                                                                                                                                                                              mitochondrion Myrmecia pilosula (Australian jumper ant)
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Crozier, R.H.
Direct Submission
Submitted (08-OCT-1994) Ross H. Crozier, School of Ge Trobe University, Bundoora, Victoria 3083, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:13618"
fissue_type="head and thorax muscle"
dev_stage="adult worker"
22. 733
88200 TATTATTTAAAATGCAATAAATTAAATTT 88233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Myrmecia pilosula"
Organelle="mittochondrion"
mol_type="genomic DNA"
gtrain="HI87-128"
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/transl_table=5
/producE=cytochrome b"
/protein_id="AAA86970.1"
/db_xref="G1:576755"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/dosg/denbank draft data.html). MOTE: This is a 'working draft' sequence. It currently consists of 10 contides. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                  Worley, K.C.
Direct Submission
Direct Submission
Submitted (19-MAR-2003) Human Genome Sequencing Center, Departmen of Molecular, and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 148444 bases at least Q40
Consensus quality: 149298 bases at least Q30
Consensus quality: 149814 bases at least Q30
Estimated insert size: 147256; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
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contig of 13738 bp in length
gap of unknown length
contig of 16666 bp in length
gap of unknown length
contig of 42787 bp in length
gap of unknown length
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contig of 2199 bp in length
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contig of 3592 bp in length
gap of unknown length
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gap of unknown length
                                                                                                                                                                   Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact project Information
Center project name: AMEK
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45.8%; Pred. No. 0.35;
tive 0, Mismatches 218;
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contig of 54896 bp
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xref="taxon:7460"
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Matches 184; Conservative
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                                                                                                                                 73323 GCTATATGTAGCGTGAAATTTATCACATGGTATGATTAATTCTTTATTGTGGAATAATTT 73264
                                                                                                                                                                                                         73263 CAATTGGTAACTTTATGTTTTTTGGAATAAATTATTAATTÄTTTTGTATAATTTTTA 73204
                    TITACTGGACCCCATTGTACAGATGGTCCCATAATAATACTGATAGAAGATAGAAGAATG 1414
                                                                                              1415 GAAAGTGATTTGTTCACGTGGTACAATCGGAATGGTTCTTTAAAGCTCATCGAACACACT 1474
                                                                                                                                                                       1475 AGGACCGTTGATTTTTCCCGCATCAAAAGCGTTGAATACTATTCTCACTTGTTTTCCTG 1534
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Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                                                                                                                                                                                                                                                                                                                                                                     AC141740 151143 bp DNA linear HTG 19-M2 Apis mellifera clone CH224-58F11, WORKING DRAFT SEQUENCE, 10
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HTG; HTGS PHASE1; HTGS DR
Apis mellifera (honeybee)
Apis mellifera
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125796 GGAAATAATTATCTTAATTTTATAATAAAAAATATAGATATAGATAAAAAATAAAATA 125855
                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 249943)
Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlon, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, T.T., James, K., Elsen, J.M., Nentherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Perea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
                                                                                                                                             AGGTATTTCATTTGGGAGTGTACTAGTAACTAGTAGTACTAACCAGAATGAGTTTCTGA 1266
                                                                                                                                                                                                                                                                                                                                   1327 AAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCAT 1386
                                               1147 AATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCT 1206
                                                                                                                                                                                                                                     1267 TTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGA 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE014823 249943 bp DNA linear INV 07-OCT-2002 Plasmodium falciparum 3D7 chromosome 14 section 8 of 13 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSKTEYDILSLVNAVEEFSKYCSEYKKRHLTNYIQSCSVKNQIN
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DKLNNENI LEDKWKRNI CEHI KSKI NDKNFVQNNDYGKNI KI INNI NEQNLLMKDKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-5EP-2002) The Institute for Genomic Research, 9712
Medical Center Er. Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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protein id="AAN37021.1"
db xref="GI:23497479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125916 ACAGATAATTAATATAATGTCATAATGAAATATAATTATTT 125957
                                                                                                                                                                                                                                                                                                                                                                                                                                1387 AATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTT 1428
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mol type="genomic DNA"
'isoTate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (<357. .>4163)
/locus_tag="PF14_0408"
complement (<357. .>4163)
/locus_tag="PF14_0408"
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chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete sequence.
AE014823 AE014187
AE014823.1 GI:23497478
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NE014823/c
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JOURNAL
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NNMDGKKNNLASNTSDFYQSISDFYKNBKNLICQEQNNNNTYIQKCAFFLASNETNV
LTNNKNHHKSGKNLISLCFDDELSSAITINNDSSLAKAIYNEFNNSEKDIVEDICNTT
NYCLINMENNTYQDDRKWNDEYCNEDYNLFRENQLKKYKELLLSCISYNEKNN
DQDRMINVEINNDFKVKNILVETNISFENGISKNHYNTINLKVIYENKYKKYN
RLAFIKGQIILLNKYKVVKULSKTQFSTTLKCLALLYKKKYKTDTQVFLPYCHKYNGXDS
RITHDKKKNNYDKFVYKNINTIKKKKCHNLIYENKKYTDTQVFLPYCHKYNGXDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="mrnvfsbapfldnnnlnkndnvlcktlltnannenertknlplkd
Rlatvrnvonllnkknlnktdeneekktlnnnfktntglentkptllnestfnrfkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYKNNIKKGVTCIPLNYQSKGGAMAIILIGTDTTYGPVKNSYGFWTFLVLDCHTNNFF
IDTGIKNNVIECEKHMOLLISPGDMYMFKNQSHEMEARLLLIVCNKOMOPFDVKMHIK
                                                                                                                                                                             LKVMKNGKOFLDOGILBIMVINILCNANTNNNILSNKNI IQLYDS FYYKEHLI I VTEYM
SOBLYMYF RKGKLGTIGOLO ILTKULBGIAPITHSKULI HODLKPBINTNINMKRKKK
NHEKGKYNKYNOKYNY INDTI EBHILINSKILBKKNI I PYSPEDOTFIEBKOP
OYDNNEKTSNVLYDSDKSYNNNVKNMI DNNLY CNNI KNI DNNSDNNNNNNNN FPHNN
                                                                                                                                                                                                                                                                                                  ÎNIYNTKQFDKIKIÎDPNSCIYESDKLEMYIQTRSYRSPEVLLQQNYDRKIDINSLGC
ILEPELTKELLDYQNIYRETYSIQSYGPPEPAYINNCHE PHETKTEALIILAKETT
DINYENYIKEEQLEDEDEEI YNENSHDFPELNKUDNIÎTKDLLAKRENPYSTPRKEN
NINBIYYDVCYPSDNLLKNNFQISDTIPYDFISSLLQIDPSKRCNAMEALKHPWLQPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YHSSGNVNNYTFSHTTSSNNNHANDNSNSQQNAKFKRKRKKKEMEBYRARLLKEKAHQ
QNSLGSILNKTNSFNKADNNSTQEBIKVKRRRGRPKASEVAAINIMNNKLKQNDIRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSVVNBKQNEELEKKLKKRKRKRYTLMERMKOKEREKRKORKUEODONGEEQYDDE
EHEEEGEDDNDDEYDRONNEOEDHFEDED YYAENDHNINNINNINININININKS FKFIRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNKYDENDFNNHKKDKGDDEEYEDDDEENDDGYDEDGGGSYKYNNNNSKDDNTFNKKN
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358. 4387
                                                                                                                                                                                                                                                                                                                                                                                                                                                       089. .1149
rpt:type=tandem
186. .4225
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locus tag="PP14 0410"
oin(9\bar{317}. .9689;9836. .11238)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="hypothetical protein"
protein id="AAN37022.1"
db xref="GI:23497480"
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complement(<5667 ...>7331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cous_tag="PF14_0409"
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/rpt_type=tandem
:352. .5382
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> xref="GI:23497481"
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543. .4577
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9797.8020
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8386 8438
/rpt_type=tandem
9083 9109
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rpt_type=tandem
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9317...>11238
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264. 9293
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LQEELLKKI PNVNNKDVSFNIYDTKKDHSLCSBALYDYMDIFKIILNKIQKDKNIHEN
LSVVNSVLILNMLSRINFCNYEIFKFFTKNYYKNLNDKDLEPHHFTLLLNSFAKCNIH
INIMKYILKYMNNKNFINNLSYVNITNAVHYMAKFNYRNATFLNHLKDKVIEIIDIIP
                                                                                                                                                              QREFSNIMWSLAKLHIKDDYFYYIAFQKIKQIIDVMDMMSVAQILDAMRRRKONSNGQ
DIGATIKEKKOLLENDISCPLADIKOTLMGQNIDYKNNIEHNKYHNDEEKVKEKEIIT
TQTTQNKDLNNNIQLTYKTPENNIISIEKNINTYNIISDLEKNILHLLVNKYIKHI
QHCSLHYULQVPFCLLLLNYINSDIYYKSLEILRKKKRNDMTTLMLIYAKYPLRIFIEK
QEAHFQKLPRSLKQFAKEILNSDNN"
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ICTRIDNIQDIAISDNNYTIYYGGBRKLIBIFDIXEENKRCNNDIGKYVDVSIPSII
KNIKLKAKGNGSESDNWKHNNILSKAALDNKYIPYHKTKYNISNGKSIYIPIINYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSICYSSLTFDLSKDKFNNILMTSGYDGYIRLYDISNNIIKSPYDEEKSITHCMFSN
NNKYIISTNKSKFGKVFDFWYMNKMNSKMMATYLMNYKTYCLNKFLIRKENLENENY
HDTINEDDIFSSQLYNDKEYALCKIGNIFSDEELEERIKIVNELNRKINEQENKHFEP
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NKODSININDINININININKONININKORININKKKYNININKYYNINIDINITYVEEDDYPESNYS
KSYPHINIPLININYHSLIDDEREPSLYYMLSEIISNEDDIPKESCIAGDKCIIPSID
TYAHYYDIYTGFHYNSIKNIYLPNYYVDNHSYYSHSIDDINKKIISFLISVDTYPKNQN
IIATSNGYPDGSIVLMAFVAR"
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VLKIWDLRMNLFNISKKSSRSNKSDIIFIDNKNPFASICSHEDTVTSITFNKTIDHEG
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translation="MRKLLSTAIMDLKKIKGNNFESKHCNDNLKSLIIKNIHKFENDE"
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/rpt type=tandem

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complement (<12999. .15334,15524. .>15647))

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complement (join(12999. .15334,15524. .>15647))

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/complement (join(12999. .15334,15524. .15647))

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db_xref="G1:23497483"
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15809. 15855
Typt_type=tandem
complement(a.17033. .>19621)
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/rpt_type=tandem
15450. .15497
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mRNA CDS gene mRNA

CDS

gene mRNA

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190126
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                  /trānslation="MSSVFNYFFKNPVLKEKRNLFFKYNILERGYSKITSVNLNNWNN IHKEIIQKINNSDRYSIDHENDEXTGLEHKDRRYISLSSYEAHOYGAKSFPRQIGISIA KKKDIVEDLYQIDERNKIKKKSSVHTKKYIYENGNNNKICNIEKKKQEWHISPYCIY VPPKENKYPSVSTGTILEKKKQEWHISPYCIY VPPKENKYPSVSTGTILSFLKENNPPRWIFWIPWGYLRPNBEBEKKKGVIVEKINBLNN LLSKCNTNKKNIIPGEKKHILDKIIQEIENYKIVDDEDKEAIISIIKKIGKHINNTNND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGAATCCTGGAAAGAGGATTATTCCATAGACACTAATTAGCTTTTTGGTGGCGCAGCC 1043
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                                                                                                                                                                                                                                                                                         803
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1 (bases 1 to 56956)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
                                                                                                                                                                                                               CGGTCGTATGTACAAGTAGCATAGCTAGTGGTTCAAACCCGGAAACAAGTACCAACGAATC
                                                                                                                                                                                                                                                                                                                                                                     AAAATAAGTTTGAATCGGTTACATCTAGTTACCGTCGAACTTACAATCATTTCGATTACT
                                                                                                                                                                                                                                                                                                                                                                                                        190125 AIGTITITITITATTATTATCIATTTTATATATATATATACAGAAAATGTATAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATATATATATATATATATATATATATAAAAAAAATTAAATTTGACCATATTTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1044 TTGTGACCTACATTAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCCATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAAAGTAAATCTTTTTGCCTA-ACCAATAAAATTATTGAAAATCTTTCCAACCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1163 GAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTATTTCATTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189825 ATTTÄTTAATTTGTTTTGAATTÄTTTTTAACCTCCTÄATAAGTAACACGTCACAATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITICITAGGITAAAAAACAAGTATATTACTAAACAATAAAAGAAAAACATTTTGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGATCIGATITICIAGITICGGITITGIATGITIAATATICCGGATIGIACAAGIACAAGI
                                                                                                                                 3.2%; Score 53.2; DB 3; Length 249943;
.larity 43.4%; Pred. No. 0.32;
Conservative 0; Mismatches 383; Indels 1;
xref="GI:23497484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189645 TAAAATTAATGITTATT 189628
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HTG: HTGS PHASE2.
Dictyostelium discoideum
Dictyostelium discoideum
                                                                                                                                                   Similarity
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AC117081
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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AC117081
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FNNKINNQVESIRIDSDFVEPIDLQNVYELTNLHTLSIPLEHQMILLALGIGGKLHCR
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VIEKNFSDKKHFQSILNDRNINGDNGLFVITVSNKKRLC"
COMPLEMENT (190117912. . 18092, 18308. . 18333))
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SATWAILSAAKGKPRTVSVTNGVIAGLAGITPSASYTNSVGSTGGTGLASYTSV
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IGVVSVAVWAAAWTWVLLKIIDATIGVKIDESBEELGLDLVEHGEFAYHNISLQGNBN
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QLSKLETEGNLKYRKIISKNPYSKOGFWAN ELEGGTAKGIEKGILDISSNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNIVELKGTAKGIEKGILDISSNNNNNNNN
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NINFILYRPKKIYDVCLHBYFKMYKWYGYSIIKINQSIIKDYFRRULGETYBK
LLQLSKLETBGNLKYKKIISKIYTKUVFKNILFLEGGIAKGIENDISSNKNNNN
NNNNNIVELIVYDFLLENDAEEGFYNLLPKEDDEYGIYKDLQPILYLNTIDYEGSQDD
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QNYYELTNLHTLSIPLHFHQMILLQLGIEBLHCRGDLLEHTDNVMQDWDKNIQSLLA
SKSIKNFRIPNKCYLGECINQSIKSYNNENYEARENSROYKKESBOIKQLLSSSTFKYF
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ELLNEIINLSNKISKVQQQQQQSIKEFKIVINKKINNKHFQTILNDRNINGDNG
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GIIGNLDHAFLINVSYDDCSPNAPNIPAAAYAFFWMMPANITPLLMTGAFAERVKFKA
FIALTVAWEIIVFYPVAHWIWGGGWLHKYFGVLDFAGGIVIHTSAGVSALVIALYVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MVAGEIIKGVAAEITNGSSSSVVQKYLDCANQVAPDPGNTTWVI"
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Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular
Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
(http://genome.imb.jena.de/dictyostelium/)
intip://www.uni-koeln.de/dictyostelium/project.shtml
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SKSNPNYTFTLSLGIPPILNLVDWQSSTTDLVIDGSFFTVNSSIINITIGNENCLVTN
          Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                 Baumgart,C.
Direct Submission
Direct Submitted (06-APR-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
3 (bases 1 to 56956)
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8472. .8483)
/note="GRF_ID:dd_02930"
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
                                                                                                                           Sequence and Analysis of Chromosome 2 of Dictyostelium
Unpublished
                                                                                                                                                                                                                                                                            Dictyostelium Genome Sequencing Consortium
(bases 1 to 56956)
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/mol type="genomic DNA"
/strain="AXA"
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join(3766. 3316,3871. .4174)
note="0RF_IDidd_02929"
/codon_start=1
/product="hypothetical protein"
/protein_id="MAM43758.1"
/db_xref="GI:21166141"
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| join(8654 . 89008 . .11010)
| join(8654 . 18006 . 9008 . .11010)
| codon start=1
| codon start=1
| product="hypothetical protein"
| protein id="hypothetical protein"
| db_xref="G1:21166142"
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/note="ORF_ID:dd_02927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="4903137-4960091"
join(33. .523,639. .263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:44689"
/chromosome="2"
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AX461144.1 GI:21726352
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                                    52986 TIT
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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SOURCE
ORGANISM
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AC004401/c
                                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
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LOCUS
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ORIGIN
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AUTHORS
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                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
| protein id="AAM43768.1"
| db xref="G1:21166121"
| /translation="MPIYFEPFHYNVTAIPDFKILTFVQYPNITIIPCKEFLSKTDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAATGGT 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PONSNINNINNINHINNISYNSGFOGDLSSYDGDWRPKETAPAMRBYLEKHEKEMOEKK
(SEEKROKKI ABAKQSLDNFYSEREAKKKTALKONNEDHNKSLETDSTSGNTTHTWES
/SMIDLQAKPNPANKDTSRMREILIRLKOYQPIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAAATC: 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 TITCCAACCAIAGAAAAGTTAAAITTGAICAGCGAIGGAAAITTITGIACAAAGCIAGGT 1210
                                                                                                                                                                                                                                        KEAIFSEDOVRFYMAELILALEHLHDSNIVHRDLKFENILLDSQHCILTDFGLÄKTE.
KYRINBETSERGTLEYMA PAM QHATOKAVOWNSIGTLIMPDMIGKEPPEHKNALM
QEKIISEKAKFPKFVSSSARGLINGLLTKDPTKRLGANGAIETKRHPFPKSIGNRKIE
NKEITPPFVPSTKGIDDISNPDHASLKAHQRDSFSTSPTLSSSQQAYFDGFSFVRTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             produčt="hypothetical protein"
protein id="AAM45766.1"
db xref="dl:21166496"
translation="MSDPFGEENVEITEEFVEGDINENDLIDGNVEYVDGNGISPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rotein id="AAM43767.1"
b_xref="C1:21166150"
ranslation="MKRFISTTSLRVLSNINKONNNNKFNKSIVGVFNREFSSSNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNKVNFGENNNSSTTEPTKVLFNDSQFYQEDKYQGISKEPPSKEIVDTLLADLNPDDI
EIKPDGLIYLPPIKXRILNQAFGPGGWALKPPGPPVVEGKTLIRPYALYCLGRYVAE
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NNNSDSSSSINQPQQETISYHQDDSSSPSSKITEQQDDSEDIDIDDVVPPQLKKYAGK
                                                                                                     translation="MTTTISSNLPSQLBISPTKLLITKQPIKLRBSTESPFKSMMDTF
                                                                                                                                      OWTIECTSPTECEESSSYTITTPSEESLSGGEESSSISDBESKIITTÄTLIKPSINVO
PSPTPLOWAAGETEIVKI SNSINLSWITIKHLVGKGGGEKVFQVVHVDT<u>OKVĄŁIKTI</u>K
CHII TAKKSVVWTLAKCILKKISHPFIVNLHYAFQNEKCLYLWDFVNGGGIFYHLO
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product="Witochondrial genome maintenance protein WGM101
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serine/threonine kinase homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(24089. .24410,24517. .24779))
/note="ORF ID:dd_02931"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52.6;
Pred. No. 0.
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                                    protein_id="AAM43765.1"
db_xref="GI:21166148"
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codon_start=1
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larity 46.6%;
Conservative
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Best Local Similarity
Matches 169; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019 ATTAGGTTCGTATCTCTTTTAACTATAAAAAAAAAAAACTATATGAAATGGATATGAAAATG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 899 TECAAACTEGAGAATEATETEAGCAFEAAACTCTACACGAAAAAAAAAAAAAAAACTEGCAFEAC
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                                                                                                                                                                                                        Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1255 ATGAGTTTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1315 AACAATAAAAGAAAACATTTTGTGAAAAAGAGAAATAAAGTTTACTGGACCCCATTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  779 GACAAGCGAAGCTACCCTTTGTGTTTGACGATCCTATAATAAAGTTTTTCACGGAAC
                                                                                                                                                                                                                                                                                                                  Budworth, P., Brown, D., Chang, H.S., Zhu, T., Han, B., Wang, X. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                  Bukaryofa, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trachec
Spermatophyta, Magnoliophyta, eudicotyledoms, core eudicots,
rosids, eurosids II, Brassicales, Brassicacese, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2000;
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                                                                                                                                                                                                                                                                                                                                                                            gene expression
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      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 47:18; Score 52:4; DB 6; Matches 151; Conservative 0; Minner 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana"
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      DNA
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                                                                                                                                                                                                                                                                                                                                        Coper.B.
Promoters for regulation of plant
Promoters for regulation of plant
Patent: WO 0198480-A 73 27-DBC-200
Syngenta Participations AG (CH)
Location/Qualifiers
Sequence 73 from Patent WO0198480.
                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis t
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codon start=1
product="puta
         repeat region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fiote="synonym: F21P24.1"
fiote="synonym: F21P24.1"
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                                                                                                                       Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 94038)
Town, C.D. and Kaul, S.
                                                                                                         9 FEE 18 MARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="ILTDDGIAIEGPVFREKNGEBMLELIPKIQVMARSSPNDKHTLY
KORTYTEPEVVAVTGGGTNDAPALHEADIGLANGIAGTBYAKKBIADVIILDDRFSTIV.
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GALALATEPPNNELMKRMPVGRRGNFITNAMMRNILGQAVYQFIIIWTLQAKGSMFQI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGSDSTLVLNTLIFNCFVFCQVFNEVSSREMBEIDVFKGILDNYVFVVVIGATVFFQ
IIIEFLGTFASTTPLTIVQMFFSIFVGFLGMPIAAGLKKIPV"
Omplement (594. .665)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGIGTLAKYWANDERVREALQIRKGSIGKWIRCNSNIHYDDDIISSIPYHMNNSINGY
RSLIYSGDHDMEVPFLATBAWIRSLNYPIIDDWRPWIINNQIAGYTWTYANTYATI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598413.
Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C.,
Sykes,S.M., Kaul,S., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Somerville,C.R. and Venter,J.C.
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Gene="At2g22950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: F21P24.2"
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product="putative serine carboxypeptidase I"
protein_id="APM14928.1"
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                                                                                                                                                                                                                                                                                                                                                               Organism="Arabidopsis thaliana"
mol_type="genomic_DNA"
collitvar="columbia"
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chromosome="2"
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yroduce=hypothetical protein"
protein id="AAF16608.2"
db_xref="GI:20197127"
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rpt_family="(TAAAAA)n"
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155. 4401
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complement(4633. .46
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AUTHORS
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  AUTHORS
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/ Cränslation="MSLTLEFLLLIVLILSHHAHSGSIVKFLPGFEGPLPPFLETGY
GGGREEWOLDFYFTKSERNREEDFLLAHSGGFGGSLTGALTGLERWOYDALKEFVYN
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SKHQOFFSNPPTYGGDSYSGMIVPPLVQEIGKGWYQINLQGYILGNPITDTESEQNYO
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AYHMKNSIDGYRSLIYNGDHDAMYPFLATQAWIRSLNYSITDDWKPWMINDQIAGYTR
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11602; 11704,11806; 11828,11912; .12013,12378; 12464,
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31.15294269_gb_AF410326.1_AF410326...

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12552...12620,12777...12798,13609...13730,14190...14303,

14407...14452,14559...14726)
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3397,20476. .20594,21039.
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protein_d="AAC17815.1"
db_xref="GI:3169172"
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complement (11836. 11877)

/rpt family="AT rich"

/rpt family="(Thin")

/rpt family="(Thin")

complement (15667. 15687)
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9116. 9138
/rpc_tamily="AT_rich"
10590. 14726
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chloroplast Eimeria tenella
Eimeria tenella
Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida, Eimeriidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLELFEKQKLKFTFSLSEKI IKKY LLFMHKYNYKKFNLINI I EIRLDNTI FNLGYSIT
I AQAKQLI I HGYPFVNFKLIKI PSFLLKKGDI ITLSPKSYY I FKLCKKNLYKKY I KNS
NIYDTI YI CKNTLI SI I YSILNI YNNNNYNNI LIMKYYSY "
                       circular INV 02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MLRYLGPKLKKLKRINIHMQPBFSTKYFILNTNKYNNKMILSFY
                                                                                                                                                                                                                                                                                        2. (bases 1 to 34750)
Cai,X. and Zhu,G.
Direct Submission
Submitted (13-JAN-2003) Veterinary Pathobiology, Texas A&M
University, 4467 TAMU, College Station, TX 77843-4467, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (13. .85)

product = rRAN-11e..5, aa.11e)

complement (246. .1754)

complement (246. .1754)

product = 165 small subunit ribosomal RNA"

/product = rENA-Ala..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="26S large subunit ribosomal RNA"
1176. 5247
product="tRNA-Thr"
                                                                                                                                                                                                                                                   genome complete sequence
               34750 bp DNA ci:
Eimeria tenella chloroplast, complete genome.
AY217738
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product="tRNA-Arg"
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'product="tRNA-Met"
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Cai,X. and Zhu,G.
Eimeria tenella plastid ge
Unpublished
                                                                                    AY217738.1 GI:31322455
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/note="RPS4"
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                                                                                                                                                                                          Eimeria.
                       LOCUS
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1845. .23969,24056. .24201,24279. .24355,24441. .24560,
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COMPLEMENT (18316. .18358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72502 AAGIGITITITITITITITITAAAACACGITAAAGAACGAAACTTGAICAGITATIA 72443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72442 GACAAGCGAAGCTACCCTTTGTTGTTTGACGATCCTATAATAAAGTTTTTCACGGAAC 72383
                                                                                                                                                                                                       GEDENVQFFYYFIKSENNPKEDPLLIMLNGGPGCSCLGGIIFENGPVGLKFEVFNGSA
PSLFSTTYSWTXMANIIFLDQPVGSGFSYSKTPIDKTGDISEVKRTHEFLQKWLSRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135 AAAATTATTGAAAATCTTTCCAACCATAGAAAAGTTAAAATTTGATCAGCGATGGAAATTT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1075 AGTATGGGCTTACAGCTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1315 AACAATAAAAGAAAAACATTTTGTGAAAAAGAGAAATAAAGTTTACTGGACCCCATTGTAC 1374
                                                                                                                                                                                      translation="MSLKIKFLLLLVLYHHVDSASIVKFLPGFEGPLPFELETGYIGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thote="synonym: F21P24.6; supported by full length cDNA:
Gres:33165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 52.4; DB 8; Length 94038;
Pred. No. 0.55;
0; Mismatches 181; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72382 GCCCTGACGGTTAATCGCATCGGTAGAAGAAGATCCGTCGA 72341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1375 AGATGGTCCCATAATAATACTGATAGAAGATAGAGCAATGGA 1416
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Best Local Similarity 47.1%;
Matches 161; Conservative
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    CDS
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LRNA

15

RESULT

t RNA t RNA

CDS

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNKYLLFWTIBOKILLIKKYSKTRAKGRIKKYKIIIIIGNKSGWFGIGCSKDYYLODA
ISKARLHAFKNIYOISLFYSNLLKNNIYIKKKFKKLYLFSYNYKIKISSSYIIRLLFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6962 TTTAATTTGAATAAATTATATTATATTCCCATTAAAATTATTATAATGAATATATT 7021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1214 TCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTTGGA 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MKVKLSIKRLCKNGFLINROKRKYIYGVKFLNITTDKNNKNLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034 TGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTATGGGGTTACAGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6842 TGGCGTAGTCAGGTAGCGCTTCTGTTTTTGGGAATAGAAGGTCATAAGGTTCAAATCCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1094 TICCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 CCBACCATAGABABGTTABATTTGATCAGCGATGGABATTTTTTGTACABAGCTAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Matches 173; Conservative 0; Mismatches 202; Indels
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                                                                                                                                                                                                                                                                                                             .0317 .1067
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                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3416. .8682
/note="RPS19"
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note="RPL16"
                                                                                                                                                                                                               6953. .7594
/note="RPL4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602. .8423
note="RPL2"
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note="RPS3"
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Search completed: February 2, 2004, 00:53:01 Job time : 6372.59 secs

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ALIGNMENTS

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thaliana stress regulated gene SEQ ID NO 3729.
                                                                                                                           thaliana; plant; gene; stress; transgenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                      Kreps J, Wang X, Zhu T;
                                                                                                                                                                                                                                                                                                                                                       PPS RES INST.
BENTA PARTICIPATIONS AG.
indard; DNA; 1677 BP.
                                                                                                                                                                                                                                                                                      2000US-227866P.
2001US-264647P.
2001US-300111P.
                                                                                                                                                                                                                                                          2001WO-US26685.
                                                              (first entry)
                                                                                                                                                           thaliana.
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) conteacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress: The present sequence is that of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office. Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses Claim 144; SEQ ID NO 3729; 577pp + Sequence Listing; English.

Sequence 1677 BP; 508 A; 292 C; 335 G; 542 T; 0 other;

Score 1677; DB 24; Length 1677; Pred. No. 0; 0; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.0%;
Matches 1677; Conservative 0 ठ

0; Gaps

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TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 240 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT

181 181

240

AAGCCTAAAAGGTTACTACCGGTTTTGACCGGTTTTATAATTTTGGTGTTTTAATTTCTAATCCC 540 AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTTAATCCC cerereresedesecedaarereraareesaaaaesresaaaceaerreserraaerrer 421 481 481

480

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9 600 099

GGATCCGTTTGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTGAGTG GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG 541 601 601

GGATCCGTTTGTTTAATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTGAGTG

541

661

AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTA 1020 1080 1021 AFFAGCFTFFFGGFGGGGGGGCCFFGGACCFACATFAFGGGGFCCAAGCCCAAGTAFG 1080 1200 1140 1320 1140 1320 1141 ATTGAAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGGGATGGAAATTTTGTAC 1200 1500 1561 ACHTHAGTAATCTCCTTGGACGTGTAAAACGATTCTTTCCCATGATGTATCS1620 840 960 840 900 006 721 IGCTIACGGICCCICTITCIGGICGGICGIAIGEACAAGIAGCAIAGCIAGTIGAIGHT 781 CCCGABACAACAACAACGAATCAAAATAAGTTTGAATCGGTTACATTAGTTACGTTAC 841) AACTIACAATCATITICATIACTITICATITICAATATICTAGITICGGITIGATATAATAT 1261 TTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAAT TCCCATAATAATACTGAAAGAAAGAAAGAGAAAGGGAAGAAA 781 CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACCGTCG 841 AACTTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATAT ATTAGCTTTTTTGGTGGGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCCAAGTATG 1141 ATTGAAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTGTAC AAAAGAAAAACCCCATTTTGTGAAAAAAGAGAATAAAGTTTTACTGGACCCCATTGTACAGGATGG 1441 TCGGAATGGTTCTTTAAAGCTCAATCGAACACACAGGACCGTTGATTTTTCCCGCATCAA 961 AAAGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACATA GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGFFFTCTCTCT GGCTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTT 106 961 1021 1081 1201 1201 1321 1381 1381 1561 1621 1621 1261 1321 721 a δ 6666 台 යි යි ઠ ð g ઠ a පු ද

AAA88782 standard; cDNA; 1483 BP AAA88782 RESULT 2
AAA88782
ID AAA
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AC AAA us-09-938-842a-3729.rng

1 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC GGTTAAGCGTTTTACTTATGGTTTATAGCAACGGAAGAATATTGCCATTGTTGGAATGC TTTTTCAGATCATCAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA Trititagarcarcaaggcrccracagarricrragggaarggrrcaggcrrrrgrra GAAATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA 1346 GAAATTGTGTTTATTGCAACAGGTAGAACATAACCATAGACAGAGGTGTATCTGAAGAGA TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT Query Match Best Local Similarity 99.6%; Matches 243; Conservative C (first entry) 241 TAAA 244 P-PSDB; AAB19718 WO200061735-A1 08-APR-1999; 19-FEB-2001 19-OCT-2000 1226 1286 121 181 61 Lin Y; ⋩ 유 ጵ ð ⋩ ð Ä 4

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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides
                                                                                                                                                 Haematopoietic cell proliferation disorder related DNA sequence #386
                                                                                                                                                                               Human, haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Braun A, Distler J, Guetig D, Howe A, Mueller J Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu J Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; SEQ ID 386; 117pp; English.
                                     ABZ10246 standard; DNA; 8056 BP
                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002; 2002WO-EP03401
                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2001; 2001US-278333P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-018942/01.
                                                                                                                                                                                                                                                                                                    WO200277272-A2
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                             16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewin A,
Pelet C,
                                                                         ABZ10246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olek A,
                   ABZ10246
                                       Novel shrunken seed gene useful for producing transgenic plants having altered production of food storage reserve material, intracellular transport of storage protein and formation of protein or oil bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of Arabidopsis thaliana SSE1 (shrunken seed) cDNA, which was isolated from a seedling cDNA library using a partial genomic clone as probe. SSE1 encodes a protein (see AAB19718) that, when expressed in a cell of a plant, modifies or alters the production of a food storage reserve material (e.g. protein, libid or carbohydrate storage reserve), facilitates the intracellular transport of a storage protein, or facilitates the formation of protein or oil bodies. The invention provides a transgenic plant (or plant cell, plant tissue, plant organ or plant component) which includes a recombinant SSE1 ransgene that modifies the production of food storage reserves, thereby increasing nutritional value. An antisense construct is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 242.4; DB 21; Length 1483;
Pred. No. 3e-46;
0; Mismatches 1; Indels 0;
                                 SSE1; shrunken seed gene; storage reserve; storage protein; oil body; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 1483 BP; 461 A; 268 C; 347 G; 407 T; 0 other;
                                                                                                                             Location/Qualifiers
122..1225
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 57; 64pp; English
Arabidopsis thaliana SSE1 cDNA
                                                                                                                                                                                                                                                                                   37-APR-2000; 2000WO-US09192
                                                                                                                                                                                                                                                                                                                        99US-0128651
                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP.
                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-679483/66.
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gens and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 cepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention on be used: for invention. Oligonucleotides from the present invention can be used: for disferentiating between healthy haematopoietic cells for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state-and/or-single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and or inferentiation can applitication of haematopoietic cell proliferation of disorder related captures, disorders related ampliferation of haematopoietic cell proliferation of haematopoietic cell proliferation of haematopoietic cell proliferative disorders. The present method enables chaptly specific classification of haematopoietic-cell proliferative disorders allowing for improved and informed treatment: of patients.

Query Match
Best Local Similarity 49.4%; Pred. No. 0.088;
Matches 131; Conservative 0; Mismatches 134; Indels 0; Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;

1405

240

1285

Gaps

1091 TITITCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATC 1150

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1466 TAAA 1469

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0; Gaps

us-09-938-842a-3729.rng

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1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACGAAATGAGTTTCTGAT 1267
1088 AGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAA 1147
                                                                 1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA 1207
                                                                                                                                                                                                        1268 TTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAACAATAAAAGAA 1327
                                                                                                  211 AAGNTITTANNANANATITTINNNANNNTAAATITTTINNTAAANANTAAANNCNTITTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cervical cancer, cytostatic, pre-malignant condition, gene therapy, ss.
                                1328 AAACATTTTGTGAAAAAGAGAAATAAAGTTTACTGGACCCC 1367
                                                                                                                                                                                                                                                                                                          Human cervical cancer marker nucleic acid 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berger A,
                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                               AAH69544 standard; cDNA; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1999; 9908-0171350.
14-MAR-2000; 2000US-0189315.
12-MAY-2000; 2000US-0203791.
09-UNN-2000; 2000US-0210600.
21-JUL-2000; 2000US-0220114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-375006/39.
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                                                                                                                                                                         1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGAAAAA 1330
   5687 ATTGAAATTTGATGATAATGATTGTGAĞTAATATAATTTGAAAATTTTTAATTGTTTAAA 5746
                                                                                                                                                                                                      (AAL07544-AAL26789) and methods of assessing whether a patient is affilted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and encoded polypeptides are also useful for isolating compounds with cytostatic polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to human breast cancer expressed polynucleotides
                                    TTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                     1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT
                                                                                                                                        New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer expressed polynucleotide 8381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                            1331 CATTTTGTGAAAAGAGAAATAAAGT 1355
                                                                                                                                                                                                                                                                             5867 AAAAAATAAAAAAAATTTAATT 5891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1516; 3695pp; English.
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ID AAL15924 standard; cDNA; 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-2000; 2000US-0192099
29-MAR-2000; 2000US-0193480
15-MAY-2000; 2000US-0205230
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2000US-0220534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200151628-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human breast
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                                    1151
                                                                                                                                                                                                                                                                                                                                                                                                   AAL15924;
                                                                                                                                                                                                                                                                                                                                RESULT 4
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                                                                                                                                                                                The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
New isolated nucleic acid for diagnosing and treating cervical car
and for assessing and detecting compounds for treating the cancer
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Pred. No. 0.096;
0; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 369 BP; 96 A; 28 C; 29 G; 172 T; 44 other;
                                                                                                                  Claim 1; Page 242; 1051pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.4%;
Matches 115; Conservative
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Gaps

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3.0%; Score 49.6; DB 22; Length 422; 42.1%; Pred. No. 0.072; cive 0; Mismatches 162; Indels 0

Best Local Similarity 42.1 Matches 118; Conservative

Query Match

Sequence 422 BP; 112 A; 32 C; 25 G; 189 T; 64 other;

Zhao X;

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1210
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                                                                                                                                                                                                                                                                                         1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAACAATAAAGAAAAA 1330
  TTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAAATC 1150
                                                                                                                                            194
                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                     74
                                              TTGTTAAAAANAAACCAAAAAAAGGTINTTTTTCCGTAGGAAAAAAATTTTTTANTTTG
                                                                                              TTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                          253 ANTICCATCONNGCATTGTTTTTANGTTTTTNCAGGCCGNNTNTTTGGANAAAAAGTNA
                                                                                                                                                                                        1211 ATTICATITGGGAGTGTACTAGTAACTAGTACTAACCAGAATGAGTTTCTGATTTT
                                                                                                                                                                                                                                                                                                                                     1331 CATTTTGTGAAAAGAGAAA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                      25
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                                              313
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1091
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ABQ67124 standard; DNA; 20933 BP BQ67124 ESULT

ABQ67124;

(first entry) 28-AUG-2002 Human angiogenesis associated polynucleotide SEQ ID NO 154

Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

antiarteriosclerotic; ds

WO200246454-A2 Homo sapiens

13-JUN-2002.

06-DEC-2001; 2001WO-EP14320.

2000DE-1061338 06-DEC-2000;

(EPIG-) EPIGENOMICS AG

WPI; 2002-500450/53,

New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer

Claim 1; SEQ ID NO 154; 41pp + Sequence Listing; German.

bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesia-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and crohn's disease. The invention relates to a nucleic acid (I) comprising a segment of 18

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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1240 Tirataaaagatatatririttatragaigigaaaragriariritaaratatritidaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopais thallana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying a stress condition; to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses
                                                                                       1091 TITITICCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAAATC
                                                                                                                                                     TITCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                           Gaps
                          Length 20933;
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0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana, plant, gene, stress, transgenic, ds
                                                           Indela
                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana stress regulated gene SEQ ID NO 338
                                                                                                                                                                                                                1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAA 1249
                                                                                                                                                                                                                                                 1300 Tritaagrigggagrararaggraarrraaarrraaa 1338
5401 A; 396 C; 5174 G; 9962 T;
                             DB 24;
                                                           69
                                           Pred. No. 0.32;
0; Mismatches
                             Score 48.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                           RESULT 7
ABZ12533/c
ID ABZ12533 standard, DNA, 2958
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                            Query Match
Best Local Similarity 56,6%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-AUG-2000; 2000US-227866P.
26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-2001; 2001WO-US26685
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-304127/34.
Sequence 20933 BP;
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Sequence 2958 BP; 828 A; 621 C; 576 G; 933 T; 0 other;

e data for this patent is not represented in the printed is based on sequence information supplied to Derwent by

The sequence data for this

the European Patent Office.

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                                                                                                                                                                                                                                                                           1348 AATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATAATAATACTGATAGAAGATAG 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker
                                                                                                                                                 351
                                                                                                                                                                                                                                                                                                                    290 GAGAAAGGTTTTTGTTGCAAATTAGTCATGAACTCACATTATCAAACGAGGTGAAATGAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag, lactation, LMFD, if at deposition; genome mapping, gene identification;
                                                                                                                                                                                                                         1228 ACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTTTGGATTTTTGAAGCTTTTTC
                                                                                                                                              410 ATTAGCAACTAGCTAGTAATAAGTGTTTTTAGTTTACAAAGTATTTTACAGGGTTCTATC
                                                                                                                                                                                       1288 ITAGGITAAAAAACAAGIATAITACIAAACAAIAAAAGAAAAACAITITGIGAAAAAGA
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine EST associated with lactation/muscle/fat deposition #5785
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                      Length 2958;
                                                                                                                                                                                                                                                                                                                                                               1408 AGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAATGGTTCTT 1454
                                                                                                                                                                                                                                                                                                                                                                                                        230 AAAACAATCCTTCGTTTGCAAGTTCAACAGTAGGCGAGACACTT 184
                                                             Indels
                  Score 47.8; DB 24;
Pred. No. 0.3;
0; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX40620/c
ID ABX40620 standard; cDNA; 516 BP.
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                  Query Match 2.9%;
Best Local Similarity 50.7%;
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAO N.
WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovine; ss; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002137139-A1
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(WARR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; Mardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; atthiitis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule acid is used for determining a level or pattern of a molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids.
nucleic acid (comprising any of the 15112 nucleic acid sequences or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1098 ATABABITABABGTABATCTTTTTGCCTAACCAATABABATTATTGABABTCTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1158 CCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTTGTACAAAGCTAGGTATTTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                          Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 46.6; DB 25; Length 516;
16.2%; Pred. No. 0.37;
Ive 0; Mismatches 179; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 516 BP; 79 A; 14 C; 18 G; 403 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA transcription associated genomic DNA #130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.2%;
Matches 154; Conservative
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ID ABK
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06-DEC-2001

AAS45323/c

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The invention relates to a mucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer; in particular an oligomerical core of 346 sequences, and an oligomer that hybridises to or is identical or peptide mucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single mucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The mucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, theoremsial disorders, particularly syndrome, cubercularly disorders, particularly syndrome, numerological disorders, procriasis, Rieger's syndrome, undemann-plot disorders, procriasis, congenital heart disease, HDR syndrome, arthritis, polyglucamine disorders, solid tumours concern. Sequences ABK28127 ABK28472 represent DNA transcription associated genomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1084 TTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATT 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1324 AGAAAAACATITIGIGAAAAGAGAAATAAAGTITACTGGACCCCATIGTACA 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids or oligomers, useful for diagnosing or treating
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49.7%; Pred. No. 0.8;
tive 0; Mismatches 146; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 259; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                            06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-UJN-2000; 2000DE-1032529.
01-SBP-2000; 2000DE-1043826.
06-APR-2001; 2001WO-EP03973
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Best Local Similarity 49.7
Matches 145, Conservative
                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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1088 AGCTTTTTCCATAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATTATTGAAA 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA involution. The sequences are useful cycle-and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CDG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing oytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or proposis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arthritis, glomerular disease, leavy body disease, arthritis,
                                                                                                                                                            Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                       Chemically pretreated complementary DNA associated with cell cycle #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10047 ААСТТАААААААСААТТТТААААТАТТАААААТАТААААССТААТТААТАТБААТТСАА
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Designing primers and probes for analysing diseases associated with eytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.
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Pred. No. 1;
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AAS45323 standard; DNA; 17848
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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Similarity 45.6%;
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                                                                                  (first entry)
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                                                                                  18-DEC-2001
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                                                                                                                                                                                                                                                                     PCR primer.
                                           AAS45323;
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of the printed specification, but was obtained in electronic came directly from WIPO at

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1328 AAACATITIGIGAAAAAAAAATAAAGTITACIGGACCCCATIGIACAGAIGGICCCATA
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ВР ABK39976 standard; DNA; 17848 RESULT 11 ABK39976/c

ABK39976;

(first 21-MAY-2002 Human chemically pretreated gene sequence #29 strand 2.

treatment; CpG; DNA methylation; cancer; tumour cytostatic, ALDH6; CYP11A; CYP11B1; CYF3A3; Driv, serve; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism ds; bisulphite Human;

Homo sapiens

WO200202806-A2

10-JAN-2002

29-JUN-2001; 2001WO-EP07470

30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826

(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

WPI; 2002-154757/20

Berlin K;

New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer

Claim 1; SEQ ID No 58; 24pp; English

The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 000693), CYPIJA (NM 000781), CYPIJBI (NM 000497), CYP3A3 (NM 000756 and NM 017460), DPYD (NM 00110), EPHXZ (NM 001995), OCHN (NM 002380), TXNRD1 (NM 001330), UGTB (NM 01996), NM 019996, NM 019901, NM 019901, NM 019902, NM 019901, NM 019902, NM 019902, NM 019902, NM 019902, NM 019902, NM 019903, NM 019903, NM 019903, NM 019902, NM 019902, NM 019903, NM 019903, NM 019902, NM 019903, NM 01990 array for analysing diseases associated with the methylation state 33 and/or detecting SNPs (single nucleotide polymorphisms) the 87 sequences. The oligomers may also be used as PCR primers; set of 87 nucleic acids and their complements is useful for diagnosis; therapy of solid tumours and cancer. The present sequence as. (CpG) the

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                                                                                                                                                                                                                                                                 Gaps
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/glutamine disorder; solid tumour.
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                                                                                                                                                      Sequence 17848 BP, 5055 A; 211 C; 3533 G; 9043 T; 6 other;
                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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Berlin K;

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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer in particular an oligomuclectide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical transcription. The set of oligomer probes are useful for detecting the cranscription. The set of oligomer probes are useful for detecting the cranscription state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription of particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary Syndrome, haemacological disorders, immunological disorders, Wardenburg cuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, methylation status disorders, myocardial infection, hypertension, anglogenesis, erpthropolesis, compension and sorders, solid tumours or cancer. Sequences ABK28127-ABX28472 represent DNA transcription associated genomic DNA molecules of the invention.

Subscribed and so this patent did not form part of the printed specification but was obtained in electronic format directly from the
                                                                                                                                                                                                             New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 38; 32pp; English
Piepenbrock C,
                                                                                                         WPI; 2002-090046/12
                                                                                                                                                                                                                                                                                                                                                                        tumours or cancer
     Olek A,
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Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T; 6 other;

1088 AGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAAATTATTGAAA 1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTGTACAAAGCTA 1208 GGTATTICATTIGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTTCTGAT 9867 ТАТААААААТТААААСАТАТТТТАААТТААСААААТТАЯТСТААТАТААААААААА 1388 ATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAAT 0; Gaps DB 24; Length 17848; Query Match 2.8%; Score 46.4; DB 24; Length : Best Local Similarity 45.6%; Pred. No. 1; Matches 164; Conservative 0; Mismatches 196; Indels 1328 ਨ ð ⋩ ન Š ų 8 ጵ ≿ Š

Haematopoietic cell proliferation disorder related DNA sequence #386 Human, haematopoietic cell proliferation disorder, cytostatic, gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia; cytosine methylation state; gene; ds.

Homo sapiens,

03-OCT-2002.

26-MAR-2002; 2002WO-EP03401.

26-MAR-2001; 2001US-278333P.

(EPIG-) EPIGENOMICS AG.

Mueller J; Lesche R, Leu ... ler V, Otto T; Berlin K, Braun A, Distler J, Guetig D, Howe A, M. Olek A, Piepenbrock C, Adorjan P, Grabs G, Leeche F. Lewin A, Lipscher E, Maier S, Model F, Mueller V, Pelet C, Schwope I, Ziebarth H; Lipscher E, Schwope I,

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides

Claim 28; SEQ ID 386; 117pp; English

differentiating between hematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contecting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagence. The method comprises contecting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AB209861 to AB211118 or represent specifically claimed nucleotide sequences from the present invention. Oligonicleotides from the present invention can be used: for differentiating between healthy hadmantopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute invention state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related polymorphisms (SNPs) of haematopoietic cell proliferation disorder related nucleotide sequences and their complements; and as primers for the ample of the nucleotide sequences from the present invention can also be used for detecting a predisposition to/differentiation between subjectic cell proliferative disorders. The nucleotide sequences from the present invention can also be used for detecting a predisposition to/differentiation of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients. present invention describes a method for detecting and

Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;

5153 5093 1137 AATTATTGAAAATCTTTCCAACCATAGAAAAGTTAAAATTTGATCAGCGATGGAAATTTTT 5212 даататтааатттттттсаааадааттаааттааатаагатсаааатттатттт 5152 TTAATTTATTTTTTTTAATTTAATTTTAAATAAATAATCAAATATTTAAATAAATTTT 1257 GAGTTTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAA Query Match
2.7%; Score 46; DB 25; Length 8056;
Best Local Similarity 50.5%; Pred. No. 1;
Matches 112; Conservative 0; Mismatches 110; Indels ઠે 심

ABZ10246 standard; DNA; 8056 BP

(first entry)

16-JAN-2003

ABZ10246;

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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy?
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                                                                                                                                                                                                                                                                                                                                                                                                           inflammation; rheumatoid arthritis; diabetic retinopathy, macular degeneration; inflammatory bowel disease; Crohn's antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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1317 CAATAAAAGAAAACATTTTGTGAAAAGAGAAATAAAGTTTA 1358
                                                      Claim 1; SEQ ID NO 28; 41pp + Sequence Listing; German.
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling as well as oligonaclectides and/or PNA-oligoners for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences of genes associated with cell signalling.

The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the Buropean Patent Office.
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Best Local Similarity 51.4%; Pred: No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL761108 267 bp DNA linear GSS 18-JUN-2002 Arabidopsis thaliana T-DNA flanking sequence GK-205F06-014511,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCGGAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCATCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                          directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used ca be found at http://signal.salk.edu/tdna_protocols.html" 75 c 51 g 105 t
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                                                                                                                                                                               /db_xref="taxon:3702"
/clone="SALK 026421.45.45.x"
/clone="SALK 026421.45.45.x"
/clone lib="Āxabidopsis thaliana TDNA insertion lines"
/note="FOR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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0
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 295.4; DB 29;
Pred. No. 1.5e-38;
0; Mismatches 1;
                                                                                                                      /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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Arabidopsis thaliana
                                    TDNA. ....
At2945680.
Class: TDNA tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                       17.6%;
ilarity 99.7%;
Conservative
   ecker@salk.edu
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Best Local Similarity
Matches 296; Conserv
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/Clone lib."Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Bases I to 278)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.
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                                                                                    Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f418. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 agsccacerrarceccaararrrrraarrrrraagsegggargeragegargeggregaara 257
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SALK 106185.39.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_106185.39.30.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 reaccestrraraartresrerraartcraarcecesarcesrrrerraaretea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GCGAGAGITGGTGGCTGCGAAATTACAACATTATCCCTCTGTGGTGGACCCGAATCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 AATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTTAAGCCTAAAAGGTTACTACCGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTTAAGCCTAAAAGGTTACTACGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 GCAAAAGTTGGTGGCTGCGAAAATTACAACATTATCCCTCTGTGGTGGACCCGAATCTGT
                                                                  Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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Strizhov, N. and Weisshaar, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                           http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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/clone="GK-205F06-014511"
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Matches 248; Conserv
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Shinn, P.

us-09-938-842a-3729.rst

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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                       Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Assusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GGTTAAGCGTTTTACTTATGGTTTATAGCAACGGAAGAATATTGCCATTGTTGGAATGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TITITCAGAICAICAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120
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/clone lib="Arabidopsis thaliana aboveground organs two
six-week old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 12,028 non-redundant expressed sequence tags from normalized size-selected cDNA libraries DNA Res. 7, 175-180 (2000)
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 233; DB 9; Length 34
Pred. No. 2.4e-28;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     'tissue_type="aboveground organs"
                                                                                                                                                                                                                                                                                              organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="APZ63b12F"
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97.9%;
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Best Local Similarity
Matches 236; Conserv
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Arabidopsis thaliana
Bukanyota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukanyota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarcophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
I (bases II to 347)
Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV521636 Arabidopsis thaliana aboveground organs two to six-week AU521636 Arabidopsis thaliana cDNA clone AP263b12F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1540 ATATATATCCTGACGAGTCACATTTAGTAATCTCCCTTGGACGTGTAACGCCGTTAAAA 1599
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/clone=184K16185.39.30.x"
/clone=184K was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                       This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of AL2945680.
Class: TDNA tagged.
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          Ecker,J.R.
Library of Insertion Mutations in the
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H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 278;
                                                                                   Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fex: 858 558 6379
Email: ecker@salk.edu
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Pred. No. 2.3e-28;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="genomic DNA"
strain="Columbia 0"
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Location/Qualifiers
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AV521636.1 GI:8681163
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ilarity 96.5%;
Conservative
          Zimmerman, J. and
Sequence-Indexed
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69
                                                            Arabidopsis Genome
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Best Local S
Matches 249
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NVS21636/c
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AV825375
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tes 167; Conserv
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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    (bases 1 to 233)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AGCTICTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGATCATTAAAGATTA
                                                                                        This is single pass sequence recovered from the left border of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 659 Kill Fax: SBS 558 659 Kill Ghall: ecker@salk.edu
                   La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 164.6; DB 28;
Pred. No. 4e-17;
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 Studies
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The Salk Institute for Biological
                                                                                                                                                                                                                                         db_xref="taxon:3702"
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                 10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                     /mol_type="genomic"
/strain="Columbia 0
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Best Local Similarity 97.7%;
Matches 167; Conservative
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Fax: 81-298-36-9060

Email: meeki@ttc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified.Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and Sall. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV825375 AFL7 Arabidopsis thaliana cDNA clone RAFL07-08-P04 5',
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                                                                                                                                                                         /db_xref="taxon:3702"
/clone="SLK 032104"
/clone="SLK 032104"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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ilarity 97.7%; Pred. No. 4e-17;
Conservative 0; Mismatches 4;
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organism="Arabidopsis thaliana"
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Plant Functional Genomics Research Group
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                                                    /mol_type="genomic_DNA"
/strain="Columbia 0"
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/db xref="taxon:3702"
/clone="RAFL07-08-P04"
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us-09-938-842a-3729.rst

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Arabidopsis thaliana (thale cress)
                                                                                            1648 CACCGTCCGTTTTCTCTCAGCTATATTTTA
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Fax: 858 558 6379
Email: ecker@salk.od**
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                       1588 ACGCCGTTAAAACGAT
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BH493162/c
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AUTHORS
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Dept. of Blochemistry & Molecular Biology
Michigan State University
124 Biochemistry, Michigan State University, East Lansing, MI 48824
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Arabidopsis thaliana
Bukaryota, Virialiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Virialiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rossid;
loases Ito 378)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Ilarduya, C., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
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/dev_etage="s-jj days after flowering"
/dev_etage="s_jdays after flowering"
/dlab_host="s_coli"
/clone_lib="Arabidopsis developing seed"
/note="crgan: Developing seed; Vector: pBluescript SK-;
Site_i: EcoRi, Site_2: XhoII"
/97 c 81 g 92 t
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                                                 SalI; subjected hr)"
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Pred. No. 0.00018;
0; Mismatches 2; Indels 0.
                                                                                                                                               Length 486;
                                                                                          3 others
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                                                                                                                                             DB 9; I
8.2e-07;
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/dev_stage="rosette plants"
/lab_host="bhl0s"
/clone_lib="RAFL7"
/note="Site_l: BamHi; Site_2: Sa
cold-treated (1, 2, 5, 10, 24 hr
a 118 c 117 g 117 t
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100.0%; Pred. No. c...
0; Mismatches
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strain="Columbia"
db_xref="taxon:3702"
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Fax: 517 353 9334
Email: benning@msu.edu
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ilarity 97.8%;
Conservative 0
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Best Local Similarity 100.
Matches 101; Conservative
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Best Local Similarity
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CGTCGTCATCTC 1647
                                                                                                                                                                                                                                                                                                                                                        GSS 30-JAN-2002
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Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directly sequenced to determine the genomic sequence at the site of insertion, Details of the protocols used can be found at http://signal.malk.edu/tdna protocols.html"
                                                       13 ACGAGGITAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTCGTCGTCATCTC
                                                                                                                                                                                                                                                                                                                                                                                       TDNA insertion lines Arabidopsis
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/clone="galk 035853"
/clone lib="Azhadopsis thaliana TDNA insertion lines"
/note="PGK was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At2945680.
Class: TDNA tagged.
Location/Qualifiers
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thaliana genomic clone SALK_035853, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                        linear
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/mol_type="genomic DNA"
strain="Columbia 0"
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Pred. No. 0.0014;
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100.0%; Pred. No. v...
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a; Tracheophyta;
eudicots; rosids
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 735)
                         GSS 13-DEC-2001
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                                                                                                                                                                                                                                                                                                                                 735 bp DNA linear GSS 13-DEC-200
BONGW95TF BO 1.6 2 KB tot Brassica oleracea genomic clone BONCW95,
B743nco.
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825 bp DNA linear GSS 13-DEC-:
BOGOH91TR BOGO Brassica oleracea genomic clone BOGOH91, genomic
BU493162
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/clone lib="BOGO"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
1 174 c 137 g 222 t
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eu
eurosida II, Brassicales, Brassicaceae, Brassica.
I (bases I to 825)
Town, C.D., Van Aken, S., Utterback, I., Koo, H. and Frass
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/strain="TO1000DH3"
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/clone="BOGOH91"
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                                                                                            BH493162.1 GI:17701266
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ilarity 80.0%;
Conservative (
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Contact: Chris Town
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                                                                           ACCESSION
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1069 ACCCCAAGTATGGGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAA 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               962 AAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTAA 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 ACCCCATGTATGGGCGTTTAGCTTTTTCCATAAGAAATCTTTAATAAAAAATTTCAACGG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            844 TIACAATCAFTFCGAFTACTFFGAFCTGAFTFFTAGTFFGGFFTFGFAFGFFTAATAFCCG 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 TTAGACTGTTTTTTTGTGGCGCAGCCTTTTGACCTACATCAAGTCATCAATGGGGTCCA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904 GATICIACAAGIACACAAGIACAIAAGIAIG--CGIAIAIGIATGIGACCGGIIIAAICA 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AAGGACG-----ATAGGATGTTGGAGCCCAGG--AGAGGATTATTCCAAAGACACTAA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 GATTGAACAGTGTTCCAAGTACAAGTATATGATTCTAAAAGGGATTAACCGGTTTAGTCC 223
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BX364179 Homo sapiens B CELLS (RAMOS CELL LINS) COT 25-NORMALIZED Homo sapiens CON 25-NORMALIZED Homo sapiens cDNA clone CSODL010YC24 5-FRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                           /clone="BONCW95"
/clone 11b="BO11.6.2 KB tot"
/note="Vector: pHOS1: Site 1: BstX1, 1.6-2 kb sheared
rotal DNA inserted into pHOS1 using BstX1 linkers"
rotal DNA inserted into pHOS1 using BstX1 linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.9%; Score 64.6; DB 29; Length 735;
Best Local Similarity 62.3%; Pred. No. 0.66; 94; Indels 24; Gaps
Matches 195; Conservative 0; Mismatches 94; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 Traacargriacrerrictagererecrivitigiarreraterrirererrica
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3185.
more information about this cluster, see
                                                                                                         provided by Tom Osborn
        MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i, W.B., Gruber, C., Jessee, J. and Polayes, D. ull-length cDNA libraries and normalization
9712 Medical Center Drive, Rockville, MD Tel: 301-836-3523 Fax: 301-838-0208 Email: cdtcwn@tigr.org DNA is from a doubled haploid provided by Seq.primer: TF Class: Sheared ends. Location/Qualifiers
                                                                                                                                                                                                                                            organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX364179.1 GI:30372792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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SOURCE
ORGANISM
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BX364179/c
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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EATURES

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A Sequence-Indexed Library of Insertion Mutations in the
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                              dopsis Genome
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                                                     Unpublished
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                              Arabi
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Matches 8
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BX335665/c
LOCUS
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ORIGIN
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JOURNAL
COMMENT
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AUTHORS
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                                                JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC459772 600 bp DNA linear GSS 03-JUN-2003 SALK 133376.34.05.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_133376.34.05.x, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1086 ACAGCITITICCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGA 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGC 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1266 ATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAG 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1326 AAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCA 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1386 TAATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGA 1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 AATTTTTTAATTTTTAATAAAAAAAAAAAATTWAAAAAHMMTTTWAAAAAAAAATTAT 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:960"
/db_xref="taxon:960"
/clone="CSOD1010YC24"
/cell_type="B_CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_type="B_CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
                                                                                                                                                                                                                                                                                                                                                              /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V stres of the pCMVSPORT 6 vector. Library was normalized. 128 c 121 g 449 t 156 others
http://www.genoscope.cns.fr/
cgj-bin/cluster=3185.r. Contact
cgj-bin/cluster.cgj?seq=C80DL010BB12QP1&cluster=3185.r. Contact
cggj-bin/cluster.cgj?seq=C80DL010BB12QP1.
fulllength.invitrogen.com/InVitroGen Corporation 1600
http://fulllength.invitrogen.com/InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : C80DL010BB12QP1.
1.01201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.8%; Score 63.8; DB 13; Length 1201; Best Local Similarity 38.9%; Pred. No. 0.78; Matches 144; Conservative 46; Mismatches 180; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                      organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  survey sequence.
CC459772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347
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1C459772/c
JOCUS
DEFINITION
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ORGANISM
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FERSION
CEYWORDS
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BX335665 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="SALK 133376.34.05.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="FCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057 TAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCCATAAAATTAAAGT---AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BB 11: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7077.f
Contact : Peng Liang Email: fliang@lifetech.com UKL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO17DE02QPI.
                                                                                                                                                                                                                                     This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 600,
Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA FIEL SBS 453 4100 x1752 Fax: SBS 558 6379 Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 Arciritinagegrarecaaraaaarianggaaaarcirtaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63.4; DB 29;
Pred. No. 1.1;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                      1. .600
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic"
/strain="Columbia 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX335665.1 GI:30308396
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87; Conservative
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clone="CS0DI017YJ04'

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BX404443 BXT 13-MAY-2003 BX404443 Homo sapiens cDNA clone CLOBB029ZG02 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                      1084 TTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATTATT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                          1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAAAACCATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCC 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="PLACENTA COT_25-NORWALIZED"
/close_lib="Homo sapiens PLACENTA COT_25-NORWALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSFORT 6 vector. Library was normalized.

126 c 198 g 381 t 144 others
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6537.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?eeq=CD0BB029ZG02FP1&cluster=6537.f. Contact
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB029ZG02FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATITITITITIANIWAAAAAWAAAAAWWAAAAAWWIWWWITITAYITAAATITIAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                          1144 GAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        965 AAAAAATACCYCCAKAAAAAATTTAAAAAATTYTAAWAAAAAATTTTCAACAWA
                                                                                                                                                                                                                                                                                     2; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     Length 1201;
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Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 37.8%; Pred. No. 1.2;
Matches 154; Conservative 63; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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KEYWORDS
SOURCE
ORGANISM
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BX404443/c
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_txref="taxon:9606"

/dlone="Cloud beloa? 1.00"

/tissue_type="NEUROBIASTOMA"

/tissue_type="NEUROBIASTOMA"

/clone lib="Homo sapiens NEUROBIASTOMA"

/note="Vector: pCW/SPORT 6; lst strand cDNA was primed note="Vector: pCW/SPORT 6; lst strand cDNA was primed oblide-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized in 194 others
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                                                                                                                                                                                                                                                                                                                 Length 936;
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                                                                                                                                                                                                                                                                                                                 3.5%; Score 59.4; DB 13;
ilarity 47.1%; Pred. No. 4.4;
Conservative 17; Mismatches 118;
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Job time : 3887,05 secs
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Matches 120;
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ORIGIN
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us-09-938-842a-3729.rni

8 37.6 2.2 8133 4 37.6 2.2 8133 4 13.6 2.2 8133 4 1 37.6 2.2 1230025 4 3 37.4 2.2 1395 1	34 37.4 2.2 1395 2 35 37.4 2.2 1395 4 36 37.4 2.2 1763 2 37.4 2.2 1763 2	337.44 344.44 444.44	42 37.4 2.2 8457 2 43 37.4 2.2 8457 4 44 37.4 2.2 14066 4	37.4 2.2	ALIGNMENTS	232-463-14/ ence 14, Ap nt No. 5670 ERAL INFORM	APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: STAKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS: ADDRESSEE: Poley & Lardner STREET: 1800 Diagonal Road, Suite 500	CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22313-0299	COMPUTER: IBM PC compatible CPERATING SYSTEM: PC-DOS/MS-DOS COPTWARE: PatentIn Release #1.0, Version #1.25	CORRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION: 435	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/935,313	; APLICATION UNMER: EP 91 114 300.6 ; FILING DATE: 26-AUG-1991	768	; REFERENCE/DOCKET NUMBER: 30472/114 IMMU ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (703)836-9300	; TELEFAX: (703)683-4109 ; TELEX: 899149 ; INFORMATION FOR SEQ ID NO: 14:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 7218 base pairs ; TYPE: nucleic acid ; STRANBEDNESS: single	inea CE: pt-F	Query Match 2.8%; Score 46.4; DB 1; I
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: February 1, 2004, 21:45:16; Search time 110.457 Seconds (without alignments) 6701.220 Million cell updates/sec	Title: Perfect score: 1677 Sequence: 1 ggttaagcgttttacttatgtttctctcagctatatttta 1677	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	hed: 569978 segs, 220	Total number of hits satisfying chosen parameters: 1139956 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	cessing: Minimu Maximu Listin	Database: Issued_Patents_NA:* 1: /cgn2_6/ptcdata/2/ina/5A_COMB.seq:* 2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:* 3: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:* 4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:* 5: /cgn2_6/ptcdata/2/ina/becTUS_COMB.seq:* 6: /cgn2_6/ptcdata/2/ina/backfiles1.seq:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description	1 46.4 2.8 7218 1 US-08-232-463-14 2 42.2 2.5 1666 1 US-08-076-090-1 3 42.2 2.5 1666 5 PCT-US94-06661-1	4 42.2 2.5 2500 1 US-08-550-715-10 Sequence 10, 5 42.2 2.5 3385 4 US-09-411-449-3 Sequence 3, 6 42.2 2.5 3385 4 US-09-411-440-1 Sequence 3, 6 42.2 2.5 3385 4 US-09-411-440-1 Sequence 3, 6 42.2 2.5 3385 4 US-09-411-440-1	42.2 2.5 3805 4 US-09-411-449-4 Sequence 1, 42.2 2.5 3916 4 US-09-411-449-2 Sequence 2,	9 42.2 2.5 6060 5 PCT-U596-09430-7 Sequence 7, 10 42 2.5 1440.5 908-09-107-5328-2589 Sequence 25: 11 39.6 2.4 837 3 US-08-998-416-288 Sequence 28:	3 39.6 2.4 7218 1 US-08-232-463-14 Sequence 3 3 2.3 731 1 US-08-451-405A-2 Sequence 4 39 2.3 2251 3 US-08-991-08-91 Sequence 5 0 3 162016 W. C.	15 39 2.3 1564976 4 US-008-915-421B-1 Sequents 2.3 1564976 4 US-08-916-421B-1 Sequents 2.3 1564976 4 US-09-434-408-3 Sequents 2.3 1569 4 US-09-434-408-3 Sequents 2.3 1569 4 US-09-434-408-3	o 38.0 2.3 1990 4 US-U9-601-198-162 Sequence 9 38.6 2.3 1990 4 US-08-961-527-232 Sequence 0 38.6 2.3 19124 2 US-08-487-8568-13 Sequence 1 38.2 2.3 731 1 US-08-451-405A-2 Sequence	8.2 2.3 19250 4 US-08-961-527-35 Sequen 38 2.3 2341 3 US-09-187-049-11 Sequen 7.6 2.2 2394 3 US-09-414-010-3 Sequen 7.6 2.2 2394 3 US-09-414-010-3 Sequen	6 37.6 2.2 8133 1 US-08-480-604A-5 Sequence 5, 7 37.6 2.2 8133 2 US-08-405-496A-5 Sequence 5,

Length 7218;

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LENGTH:
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                                                                    138 AACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGATAAGCTTCTCTATGTCT 197
                                                                                                                                                               198 AAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTAAATGGTTTGTAAGAA 257
                                                                                                                                                                                                                                                          378 AIGGIAGGCAAAAGTIGGIGGCIGCGAAAATIACAACATIAICCCICCIGIGGIGGACCCG 437
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Beta-Globulin Gene and Beta-Locus Control Region
Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 AATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTTAAGCCTAAAAGGTTACT
                             0; Gaps
Best Local Similarity 12.9%; Pred. No. 0.019;
Matches 59; Conservative 189; Mismatches 210; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,090
FILING DATE: 19930611
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1100 Peachtree Street, Suite 2800
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NAME: Pabet, Patrea L.
REGISTRAINON NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 6128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08076090
Patent No. 5631162
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London, Irving M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (404) 815-6508
TELEPAX: (404) 815-6555
INFORRATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuan, Dorothy
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TITLE OF INVENTION: Bet
TITLE OF INVENTION: DER
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick
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ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATTACTAACAATAAAAGAAAAA 1330
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Beta-Globulin Gene and Beta-Locus Control
Derivatives
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Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.2; DB 1;
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                      NAME/KEY: misc signal
LOCATION: 299.1148
OTHER INFORMATION: /note= "Intron 2"
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1502...1643

OTHER INFORMATION: /note= "Exon I"
US-08-076-090-1
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APPLICATION NUMBER: PCT/US94/06661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1331 CATTTTGTGAAAAGAGAAATAAA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9406661
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 ATTGCGGAGAAGAAAAAAAAA
                      TUPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                             ORGANISM: Homo sapiens
CELL TYPE: Beta-globin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1149...1370
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1371..1501
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                     LOCATION: 37..298 OTHER INFORMATION: /note=
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TITLE OF INVENTION: BEC.
TITLE OF INVENTION: DEC.
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy di
                                                                                                                                                                                                                            NAME/KEY: misc signal
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc signal LOCATION: 1149..1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc signal LOCATION: 1502..1643
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
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Best Local Similarity
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1210

803

1270

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single
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APPLICANT: James E
             Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY;
; LOCATION:
US-08-550-715-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       744 AATTGAAAATAAAGAAATAAAGTAGGGAGATTATGAATATGCAAATAAGCACACATAT
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APPLICANT:
BOWLe, Lemuel J.
TITLE OF INVENTION: Human '-Thalassemia Mutations as a Predictor of
TITLE OF INVENTION: Blood-Related Disorders
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.2; DB 5; Length 1666;
Pred. No. 0.14;
0; Mismatches 138; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE:
NAME/KEY: misc signal
LOCATION: 1371_1501
OTHER INFORMATION: /note= "Intron 1"
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc signal
LOCATION: 37..298
OTHER INFORMATION: /note= "Exon III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc signal
LOCATION: 11497.1370
OTHER INFORMATION: /note= "Exon II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_signal
LOCATION: 1502..1643
OTHER INFORMATION: /note= "Exon I"
CT-US94-06661-1
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Sequence 10, Application US/08550715
Patent No. 5750345
FILING DATE: 10-JUN-1994
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1666 base pairs
TYPE: nucleic acid
STRANDEDNESS: 9ingle
TOPOLOGY: Innear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                               CELL TYPE: Beta-globin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_signal
LOCATION: 299. 1148
OTHER INFORMATION: /note=
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Best Local Similarity 47.5%;
Matches 125; Conservative
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ORGANISM: HOR
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NAME/KEY:
LOCATION:
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1596 TGTGTACACATATTAAAACATTACACTTTAACCCATAAATTATGTATAATGATTATGTATC 1537
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TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING
TITLE OF INVENTION: Beta-GLOBIN REGULATORY ELEMENTS
THE REPREDICE: 17860017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1536 AATTAAAAATAAAGAAAATAAAGTAGGGAGATTATGAATATGCAAATAAGCACACATAT
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Pred. No. 0.16;
0; Mismatches 3138; Indels 0
                                               OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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join(687..778, 909..1131, 1982..2107)
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CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 2,246,005
NUMBER OF SPO. 7-
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IY: United States of America
60606-6402
                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,715
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Patent No. 6524851
                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIG A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.5%;
Matches 125; Conservative
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Query Match
Best Local Similarity
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APPLICANT: James E
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US-09-411-449-2/c
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SEQ ID NO 2
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TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING
TITLE OF INVENTION: beta-GLOBIN REGULATORY ELEMENTS
FILE REFERENCE: 17860017
CURRENT APPLICATION NUMBER: US/09/411,449
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 2,246,005
PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 4
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2.5%; Score 42.2; DB 4; Length 3496;
Best Local Similarity 47.5%; Pred. No. 0.18;
Matches 125; Conservative 0; Mismatches 138; Indels 0
                                                                                                                                 Length 3385;
                                                                                                                                                                                Indels
                                                                                                                                 Score 42.2; DB 4;
Pred. No. 0.18;
0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1888 ATTGCGGAGAAGAAAAAAAGA 1866
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                                                                                                                                 1.13rity 47.5%;
Conservative
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SEQ ID NO 1
                   LENGTH: 3385

TYPE: DNA

CRGANISM: Homo sapiens
US-09-411-449-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                    Query Match
Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: James E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .09-411-449-1/c
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SEQ ID NO 3
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APPLICANT: James Ellis
TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING
TITLE OF INVENTION: HEAG-GLOBIN REGULATORY ELEMENTS
FILE REFERENCE: 17860017
CURRENT APPLICATION NUMBER: US/09/411,449
CURRENT APPLICATION NUMBER: 2,246,005
PRIOR APPLICATION NUMBER: 2,246,005
PRIOR FILING DATE: 1998-10-01
                                                                                                                                                                                                                            TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING TITLE OF INVENTION: Deta-GLOBIN REGULATORY ELEMENTS
FILE REFERENCE: 1786017
CURRENT APPLICATION NUMBER: US/09/411,449
FILE REPLICATION NUMBER: 2,246,005
PRIOR APPLICATION NUMBER: 2,246,005
PRIOR PILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 4 - 0.01
SEQ ID NO 4
LENGTH: 3805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTGTGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42.2; DB 4; Length 3
Pred. No. 0.19;
0; Mismatches 138; Indels
1999 ATTGCGGAGAAGAAAAAAAAGA 1977
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Patent No. 6524851
                                                                                                        :-09-411-449-4/c
Sequence 4, Application US/09411449
Patent No. 6524851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%;
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Best Local Similarity 47.5°
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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Match		ν.	0	_	٥	_	•	_	0	~	0		RESULT US-09-1	Seque	da B																			-	Ž							
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α	,	AATTA	AATG	3TAC	ATAAG	GAGT	AAGTI	CAATA	GTAT																																6060	
Tach	1	AAAAITAAAGTAAAICTTTTTTGCCTAACCAATAAAATTA	TGTGTACACATATTAAAACATTACACTTTAACCCCATAAATATGTATAATGATATGTATATGTATATGTATATGTATAT	TTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT	aattaaaataaagaaaataagtagggagattatgaatatgcaaataaggacacatat	CTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT	ATTCCAAATAGTAATGTACTAGGCAGACTGTGTAAAGTTTTTTTT	GGATTTTGAAGCTTTTCTTAGGTTAAAAAAAGTATATTACTAAACAATAAAAAAAA	ATCTCAGAGATATTTCCTTTTGTTATACACAATGTTAAGGCATTAAGTATAATAGTAAA						တ္																										Length	
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ς. α	í	CCTA	CATA	GATG	TATG	TACT	AAAG:	GTAT	GTTA						INOP/								#																		DB 5	4
Mismatohea)	TTTG	AACC	CAGC	AGAT	TAAG	GTGT	ACAA	CAAT						HEMOGLOBINOPATHIES					-			Version	1																	C	>
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92) }	ATTA	ATTA	GAAA	AAAGA	ATTTCATTTGGGAGTGTA	LAATG	TITI	ATTTC	CATITIGIGAAAAGAGAAAIAAA				PC/1	Peter M. TREATMENT	23		Park	n		FORM:	py disk compatible	PC-1	Æ		í	DATA: SER: US	07-JUN-1995	<u>ы</u>	R: UMBEI	FORM	6997	NO:	6060 base pair	d ble	(o though)	, ,		sapiens	: 11	2.5%;	,
evitevreenoo	3	ATAA	ACAT/	CCAT	AATA	TTGG	ATAG	GAAG(AGAT	TGAA	AGAA(ication	. H Z	NCES:	OncorPharm	200 Perry	ng		E FO	ဗိုင်	-	NO	MBER	<u></u>	MBER	D-70	Glen	OMBE ET N	NI S	301-208-6997	FOR SEQ ID NO: CHARACTERISTICS	base	acid double	lear AMG	NO		ME:	MENT	}	ن بر
i d		TTTTCCAT	GTAC	CCAA	TAAA	TCAT	CCAA	TTTI	TCAG	TITG	- 99099		٥	11ca	: Glazer	OUEN	9	00 P	Maryland	S .	DABL	E: H	SYSTEM:	ICAT	Z E	NOH	N	CE:	ta,	TON N	ATIC	301-	FOR SEQ	5060	nucleic DNESS:	lin PF.	. }	SOURCE:	Homo	3/SEG	1 04miloviti	17077
	` 1											и.	-09430-7/c	7, Applicat	AT:		SSEE:			KY: L 20877	COMPUTER READABLE	M TYE TER:		APPI	APPLICATION NUMBER: FILING DATE:	CLASSIFICATION:	TOR APPLICATION DATA	FILING DATE: 07-JUN-1995	Kaı	REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:	TELECOMMUNICATION INFORMATION	AX:	ON E		- 2	OGY: 1		NSE: L SOI	ISM:	CHROMOSOME/SEGMENT: 6-09430-7	ъ 64 m.i	Q + E:
		1091	2659	1151	2599	1211	2539	1271	2479	1331	2419		- 094			BER (ADDRESSEE	TREET	TATE:	COUNTRY: ZIP: 20	PUTE	MEDIUM TY COMPUTER:	OPERATING	CURRENT	PPLI	LASS	OK A. PPLI	FILING	AME:	EFER	ECOM	TELEFAX:	INFORMATION SEQUENCE	LENGTH:	TYPE: STRAN	TOPOLO	OTHE	ANTI-SENSE: ORIGINAL SO	ORGANISM:	CT-US96-09430-7	/ Match	200
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uence 2889, Application US/09107532A
ent No. 6583275
ENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                                                                                                                                                                                                            3036 AAİTTAAAATAAAAAAAAAİAAAİTAAGGGAGATTAİTGAATAİGCAAAİAAGCACACATAİ 2977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2916 ATCICAGAGAIAITITCTITIGITATACACAATGITAAGGCATTAAGTATAATAGTAAAA 2857
                                                                                                                                                                           1151 TITCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT 1210
                                                                                                                                                                                                                                                                                              1211 ATTICATITGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT 1270
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                                                                                                                                                                                                                                                                                                                                                                                                           1271 GGATTITIGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAAAA 1330
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                                                        1091 TITITICCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATC 1150
                                                                                                                3096 igrigiacacarariaaaacarracacriraacccaraaarargrarargarrargraric 3037
0; Gaps
   0; Mismatches 138; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE, GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Waltham
STATE: No Beaver Street
COUNTY: USA
ZIP: 0234
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «UNKNOWN»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
RILING DATE: 30-Jun 1998
FILING DATE: 30-Jun 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke.
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2856 ATTGCGGAGAAAAAAAAAAA 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1331 CATTTTGTGAAAAGAGAAATAAA 1353
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELBFAX: (781)893-827'
NFORMATION FOR SEQ ID NO: 2589
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: doubl
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   hes 125; Conservative
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-107-532A-2589
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us-09-938-842a-3729.rni

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Best Local Similarity 45.7 Matches 138; Conservative
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STRANDEDNESS:
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                                                                                                                         162 ATCTGAACAAGAAATCAAAGAGGCAGATGCATCATTCTTGCAGTAGATAAAGAAATCGA 221
                                                                                                                                                             102 AAGAAATCTAAACCATCAAGCAAAATTTGAAAACAGAGGTGTAAAAACAGAAAATCAGTT
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                                                                                        Gaps
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                                                    Score 42; DB 4; Length 1440;
Pred. No. 0.15;
0; Mismatches 70; Indels
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TELECOMMUNICATION INFORMATION:
TELEFHONE: 919-541-8587
                                                                                                                                                                                                                                                                  1417 AAGTGATTTGTTCACGTGGTACAATCGGAATGGT 1450
                                                                                                                                                                                                                                                                                                      ATTGGACCGATTTGCCGGGAAAAAGTAAAGCGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6239264artis Corporation
   ; SEQUENCE DESCRIPTION: SEQ ID NO: 2589:
US-09-107-532A-2589
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/ENTION: GENOMIC DNA SEQ!
/ENTION: AND USES THEREO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: No. 6239264th Carolina COUNTRY: USA ZIP: 27709 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                            288, Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 nilippsen, Peter
                                                      Query Match 2.5%;
Best Local Similarity 54.5%;
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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nucleic acid
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.08-998-416-288/c
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BENERAL IN
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Length 837;

DB 3;

2.4%; Score 39.6;

Query Match

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1331 CATTITGIGAAAAGAGAAATAAAGTITTACTGGACCCCCATTGIACAGATGGICCCATAATA 1390
                                                                                                                                                                                                                                                     1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT 1270
                                                                                                                                                                                                                                                                                                                                                 1091 TITITCCATAAAATTAAAGTAAATCTTTTTGCCTAACCAATAAAATTATTGAAAATC 1150
                                                                                                                                                                                                                                                                                                  422
                                                                                                                                                                                                                                                                                                                                                                                           421 ARTATTTATAAAATAGATATTATAATAAAATAATAATTTACAATATTTAAATTA 362
                                                                                                             1151 TITCCAACCATAGAAAAGTTAAAITTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                                                                                                                                                                                  481 AAGTTAAAATTAATTAATAATAATTCTTATAAAAAGATTAAATAATAATAAATCAACAT
45.7%; Pred. No. 0.53;
tive 0; Mismatches 164; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKURER, F. G.
APPLICANT: FALKURER, F. G.
NUMBER OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Foley & Lardner 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: EP 9
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703,633-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/08/916,421B
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                   1331 CATTTTGTGAAAGAGAATAAA 1353
                                                                                                                                                                                                                          310 AAAAAATTAAAATCAAAAAA 332
                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08991677A Patent No. 6252135 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome-
PARENT NO. 6503729
TITLE OF INVENTION: jannaschii
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Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.0%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PB275
                                                                                                                                                                                                                                                                                                             JS-08-991-677-11/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 11
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                                                                                                                                                              1457 AAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCATCAAAAAGCGTTGAATACTA 1516
                                                                                                                                                                                                1015 ACGCTCACAGAATTAATTCCGAGCTTGGCTGCAGGTCGAGGGTTGCGATYYYYYYYY 1074
                                                                                                                                                                                                                                               1517 ITCTCACTTGTTTTCCTGCTCCTATATATATATCCTGACGAGTCACATTTAGTAATCTCC 1576
                                                                                                                                                                                                                                                                                   TTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTC 1636
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0
                                                                                 2.4%; Score 39.6; DB 1; Length 7218; 10.9%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: FASEL, NICOLAS JOSEPH
APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 731;
0.72;
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Pred. No. 0.72;
0; Mismatches 140; Indels
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                           1637 GTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTT 1676
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
                                                                                                                         85;
                                                                                                                       24; Conservative 111; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: PENNSYLVANIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 15219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Mixto 486-50
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/451,405A FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08451405A Patent No. 5736358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07/965,273
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Best Local Similarity 46.8%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-JAN-1993
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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IMMEDIATE SOURCE:
CLONE: DTZgpt-F1s
IS-08-232-463-14
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Matches 24; Conserv
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IS-08-451-405A-2
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                                                                                   Query Match
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Sequence of the Methanogenic Archaeon, Methanococc
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1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTACTAACCAGAATGAGTTTCTGATTTT 1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  795
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                                                                                                                                                       854 tritaaaatraatritroctaaatritraactraaatataagataaaatritaccaacaart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794 rittaaaaitaaragigirraaritartitraarritigaarititracroraaritraaca
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APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TILLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REPERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
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Pred. No. 1.1;
0; Mismatches 155; Indels
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PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 1664976
TYPE: DNA
ORGANIEM: Methanococcus jannaschii
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FION: (191995)..(191995)
R INFORMATION: n equals a, t,
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RMATION: n equals a, t,
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INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
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RMATION: n equals a, t,
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INFORMATION: n equals a, t,
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OCATION: (234187)..(234187)
THER INFORMATION: n equals a,
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INFORMATION: n equals a,
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FION: (234614)..(234814)
R INFORMATION: n equals a,
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INFORMATION: n equals a,
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FION: (84808)..(84808)
R INFORMATION: n equals a,
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MATION: n equals a,
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LOCATION: (28222)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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ION: n equals a,
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CATION: (84773)..(84
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FION: (84812),,(84
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TTON: (231
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INFORMAT
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KEY: misc feature ION: (1130881)..(1130881) INFORMATION: n equals a.t.c. or g c, or g KEY: misc_feature 10N: (1110988)..(1310988) : INFORMATION: n equals a, t, c, or g KEY: misc_feature 10N: (1313224)..(1313224) : INFORMATION: n equals a, et, c, or g c, or g о и в מ or g or g or g or g ö OL Ö 9 ö 9 ö c, or ä ú NAME/KEY: misc_feature
LOCATION: (312993). (312993)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (319226). (319226)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
LOCATION: (559167). (559167)
OTHER INFORMATION: n equals a, t, c EX: misc feature CON: (1084830)..(1084830) INFORMATION: n equals a, t, KEY: misc_feature. ION: (855539)..(855539) INFORMATION: n equals a, t, /KEY: misc feature
rION: (1119881)..(1119881)
? INFORMATION: n equals a, t, LEA LILL.

CATION: (600992)...(600992)
HER INFORMATION: n equals a, t,
AEVEX: misc. feature

CATION: (622708)...(622708)

THER INFORMATION: n equals a, t

AME/KEY: misc. feature

AME/KEY: misc. feature KEY: misc feature ION: (871619)..(871619) INFORMATION: n equals a, KEY: misc feature ION: (1096846)..(1096846) INFORMATION: n equals a, AME/KEY: misc feature OCATION: (1349473)..(1349473) THER INFORMATION: n equals a, AME/KEY: misc feature OCATION: (713652)..(713652) THER INFORMATION: n equals a, GY: misc_feature ION: (779676)..(779676) INFORMATION: n equals a, ON: (779455)..(779455) INFORMATION: n equals a, INFORMATION: n equals a, AME/KEY: misc feature OCATION: (559241)..(559241) THER INFORMATION: n equals a, PAME/KEY: misc_feature (657203) (657203) (10FORMATION: n equals a, or; misc feature on: (674737) ION: (741684)..(741684) INFORMATION: n equals a, misc feature (1119881)..(1119881) ION: (657081)..(657081) INFORMATION: n equals a, /KEY: misc feature FION: (682442)..(682442) R INFORMATION: n equals a, OCATION: (1349491)..(1349491) ION: (674435)..(674435) INFORMATION: n equals a, eature eature feature AME/KEY: misc ÆY: CATION

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COCATION: (1603734)...(1603734)

THER INFORMATION: n equals a, t, c, or g

AAME/KEY: misc feature

CCATION: (1637998)...(1637998)

THER INFORMATION: n equals a, t, c, or g

AAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, c, or g
    c, or g
                                                                                                    COCATION: (1559020) ... (1569020)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature
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n equals a, t,
                             LOCATION: (1470091)...(1470091)
OTHER INFORMATION: n equals a, t,
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1025747 AATTATATTATATTGCATGATTGACAATTAAAAAAGATAGCTCCTATTTTGATAATGAT 1025806 1131 AATAAAATTATTGAAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAA 1190 0; Gaps Query Match 2.3%; Score 39; DB 4; Length 1664976; Best Local Similarity 48.4%; Pred. No. 9.6; Matches 108; Conservative 0; Mismatches 115; Indels 0;

1025807 Arriarciaraarriraciarriccirragricirraaaaracaciddagacarcar 1025866

1311 ACTARACARTARARGARARACATTTTGTGARARGAGAGARATARA 1353

1025927 AAAAAGCAAATGTTAAGAAAATACTGCAAATACAACAAGAAA 1025969

Search completed: February 2, 2004, 03:00:22
Job time : 121.457 secs

Sequence 2829, Ap Sequence 4676, Ap Sequence 4038, Ap Sequence 4038, Ap Sequence 4038, Ap Sequence 4038, Ap Sequence 1328 Ap Sequence 1328, Ap Sequence 1280, Ap Sequence 1338, Ap Sequence 134, App Sequence 134, App Sequence 164, App Sequence 164, App Sequence 164, App Sequence 164, App Sequence 164, App Sequence 164, App Sequence 1788, Ap Sequence 164, App Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 1788, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, Ap Sequence 218, App Sequen

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                                                                                                                                                                                                                                                       2434939 seqs, 1822278265 residues
                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NA:*
| cgn2_6/ptodata/2/pubpna/US07
| cgn2_6/ptodata/2/pubpna/PCT i /cgn2_6/ptodata/2/pubpna/US06
| cgn2_6/ptodata/2/pubpna/US06
                                                                                      February 1, 2004, 21:42:55
                                                         - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

- F Library	US-09-938-842A-3729	; Sequence 3729, Application US/09938842A ; Patent No. UG20020160378Al	, GENERAL INFORMATION: APPLICANT: Harner, Jeff.	, APPLICANT Kreps, Joel	; APPLICANT: Zhu, Tong	, TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANS	; FILE REFERENCE: CELL STATE OF STATE O	CURRENT FILING DATE: 2001-08-24	PRIOR APPLICATION NUMBER: US 60/227,866	; PRIOR APPLICATION NUMBER: US 60/264,647	; PRIOR APPLICATION NUMBER: US 60/300,111	; PRIOR FILING DATE: 2001-06-22	; SEQ_ID_NO_3729	TYPE. DNA	; ORGANISM: Arabidopsis thaliana			Best Local Similarity 100.0%; Fred No. 0; Matches 1677; Conservative 0; Mismatches 0; Indels		Oy 1 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCA	Db GGTTAAGCGTTTTACTTATATGCAACGGAAGAATATTGCC		61 TITITICAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGTTTTT	CT THE PROPERTY OF THE PROPERT	
. seq:		. seg: * B. seg: *	MB.seq:* MB.sec:*	B.seq:*	15.8eq2:*)MB.8eq:*	MB.seq:*			ited by chance to have a control of the result being printed,	ibution.			Description	Sequence 3729, Ap	Sequence 3729, Ap		Sequence 2, Appli	Sequence 1; Appl1 Sequence 338, App	Sequence 338, App	Sequence 5785, Ap	Sequence 39, Appl			Sequence 233686,	
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*/cmm7_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*/cmm7_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*/comm7_6/ptodata/2/pubpna/	6/ptodata/2/pubpna/fcilos_fobcomb.seq. 6/ptodata/2/pubpna/US08_NEW_PUB.seq.	6/ptodata/2/puppna/US08_PUBCOMB.seq:* 6/ptodata/2/puppna/US09A_PUBCOMB.seq:*	_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:* _6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*	6/ptodata/2/pubpna/US09 NEW PU	_6/ptodata/2/pubpha/usus_nsw_ru _6/ptodata/2/pubpha/US10A_pUBCO	6/ptodata/2/pubpna/US10B_PUBCOMB.seq	'cgnz_c/ fromcu, z/ function of or o	_o/prodara/z/pubbila/useu_rubcom	.d 0		SUMMARIES		Length DB ID	10 US-09-938-842	1677 12 US-09-938-842A-3729	12	13 US-10-312-84	573778 13 US-10-31Z-841-1 2958 10 US-09-938-842A-338	US-09-938-8427	0 6	13.	15 US-10-239-676-		US-10-027-632-	
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Db 1201 AAAGCTAGGTATTICAFTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGT 1260 Oy 1261 TICTGAFTTTGGAGCTTTGAAGCTTTGGAAGAAAAAAAAGTATACTAAAACAAT 132	Db 1261 TECTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATACTAAACAAT 1321 Ob 1331 ABAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1321 AAAGAADAACATTTT	DD 1381 TCCCATAATATACTAATACAAGATAGAGAATGGAAAGTATTGTTCACGTGGTACAA 144	1441 TCGGAATGCTTCTTTAAAGCTCATCGAACATT	1501 AAAGCGTTGAATACTATCTCACTTGTT 1501 AAAGCGTTGAATACTATTCTCACTTGTT	1561 ACATTTAGTAATC	GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTA 1	RESULT 3 V V V V V V V V V V V V V V V V V V	; GENERAL INFORMATION: ; ADPLICANT: Blown:h, P. ; APPLICANT: Chang, H.	A	; TITLE OF INVENTION: Promoters for regulation of plant expression ; FILE REFERENCE: 1360.001UG1 ; CURRENT APPLICATION NUMBER: US/09/887,576 ; CURRENT FILING DATE: 2001-06-22	PLICATION NUMBER LING DATE: 2000- PLICATION NUMBER LING DATE: 2000-	APPLICATION NUMBER FILING DATE: 2000- OF SEQ ID NOS: 87	. 73 73 ¥. ¥. 8	6-73 h Similarity	es 161; Conservative C	Db 1019 AFFAGGITCGFATCT-CHTAACATAAAAAAAAAAACTATATGAAAGGATATGAAATG 960 Oy 1135 AAAATTATTGAAAATCTTTCCAACCATAGAAAAGTFAAATTTGATCAGCGATGGAAATTT 119	Db 959 AGAAATTGAAGTACGAAAGGCTCCTAAACTGTTCCTATTTATT
	181 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 240 	241 TADANGGTTIGIAAGAAATACTACATTATTIAIGTGAAATIGIGTGGTGAAAAGT 300 241 TADANGGTTIGIAAGAAATACTACACTTATTIANGTGAAATIGIGGTTAGTGAAAAGT 300	301 AAAAACATCGGAATCCAAAACTCCAAATTTACCAATCAGCCCAAATTATTGATGCTGGGG 360	361 TAATGAATGGTATGCTGATGGTAGGCAAAGTTGGTGGCGGAAAATTACAACATTAC 420 111111111111111111111111111111111111	421 CCTCTGTGGTGGACCCGAATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTT 480	481 AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCCC 540 481 AAGCCTAAAAGGTTACTACCGGTTTGACGGGTTTATAATTTGGTGTTTAATTCTAATCCC 540	541 GGATCCGTTTGTTTGATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTGAGTG 600 541 GGATCCGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTTGAGTG 600	601 GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTTAGCCCTCAACAATGTGTGGAACTGAAG 660 	661 AGAGTAGGGTCCAGGCCCACATTCACATTTTCGTTTTGTAGCCTTTCTTT	721 IGCTTACGGTCCCTCTTTCTGGTCGGTCGTATGTACAAGTAGCTAGTGGTTGAAA 780. 721 IGCTTACGGTCCCTCTTTCTGGTCGGTCGTACAAGTAGCAAGAGTAGCTAGTGGTTCAAA 780	781 CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACCGTGG 840 	841 AACTTACAATCATTTGGATTACTTTGATCTGATTTCTAGTTTGTTT	901 CCGGATTGTACAAGTACACAAGTACATAAGTATGCGTATATGTATG	961 AAAGGACGAACGATGAGGAATTTGGAATCCTGGAAAGAGATTATTCCATAGACATTA 1020 961 AAAGGACGACGACGATGAGAGATTTTGGAATCCTGGAAAGAGATTATTCCATAGACACTA 1020	1021 ATTAGCTTTTTGGTGGCGCGGCCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTATG 1080 1021 ATTAGCTTTTTGGTGGCGAGCCTTGTGACCTACATTAATGGGGTCCAAGTATG 1080	1081 GGCTTACAGCTTTTCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATT 1140 	1141 ATTGAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCACGATGGAAATTTTTGTAC 1200 1141 ATTGAAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGGGATGGAAATTTTGTAC 1200	1201 AAAGCTAGGTATTTGATGTGTGTGTACTAGTAACTAGTAAGTA

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NAME/KEY: unsure
LOCATION: (379615)
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AGTAAGTACTAACCAGA 1254
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                                                                                                      839 AAGTGTTTTTTTTTTTTTTTTTTTTAAACACGTTAAAGAACCGAAACTTGATCAGTTATTA 780
                              899 ricabactróagaariarriagcarraaacrcracagababababaaaacrrocarrac 840
                                                                                                                                                                           779 GACAAGCGAAGCTACCCTTTGTGTTTGTTGACGATCCTATAATAAAGTTTTTCACGGAAC 720
                                                                   IGAAGCITITCITAGGTTAAAAAACAAGTATATTACTA
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ASSESSMENT, PREVENTION, AND
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                                                                                                                                                                                                                                                 719 GCCCTGACGGTTAATCGCATCGGTAGAAGAAAGATCCGTCGA 678
1195 TIGTACAAAGCTAGGTATTTCATTTGGGAGTGTACTAGTAAC
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42.1%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRRENT APPLICATION NUMBER: US/10/199,846
URRENT FILING DATE: 2002-07-18
AIOR APPLICATION NUMBER: 60/306,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                        pplication US/10198846
JS20030099974A1
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Best Local Similarity 42.1%
Matches 118; Conservative
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INFORMATION: n =
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ENGTH: 858
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1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA 1207

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REPRENCE: BC1/1208/W0
CURRENT APPLICATION: NUMBER: US/10/312,841
NUMBER OF SEQ ID NOS: 2
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
PILE REPRENCE: 801/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
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322 CHNNNCANAARTTAAANTNTTTTNGTTNAAAAAAAAAAAANANTTNTTTTAATTTTT 263
                                                            1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGAT 1267
                                                                                                                                                                                                                                                   262 AAGNTTTTANNANALTTTINNANNNTAAATTTTTINNTÄÄANÄYTÄAANNCNTTTTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1156 AACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTATTTC
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                                                                                                                                                                                                                                                                                                                    1328 AAACATTTTGTGAAAAGAGAATAAAGTTTACTGGACCCC 1367
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.9%; Score 49.2; DB 13;
Best Local Similarity 49.2%; Pred. No. 19;
Matches 129; Conservative 0; Mismatches 133;
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Publication No. US20030186277A1
GENERAL INFORMATION:
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIP1300-3
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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    410 ATTAGCAACTAGCTAGTAATAAGTGTTTTTAGAAGTATTTTACAAAGTATTTTACAGGGTTCTATC 351
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                                                                                 1288 TTAGGTTAAAAAACAAGTATATTACTAAACAATAAAAGAAAAACATTT
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Pred. No. 1;
0; Mismatches 112; Indels
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PRIOR FLING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-06-22
NUMBER: OF SEQ ID. NOS: 5379
SEQ ID NO 338
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US20020137139A1
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Best Local Similarity 50.7%;
Matches 115; Conservative
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Byatt, John C.
Mathialagan, Ne
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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APPLICATION NUMBER: US 60/264,647
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CATION NUMBER: US 60/300,111
IG DATE: 2001-06-22
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US20020160378A1
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ORGANISM: Arabidopsis thaliana
                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 50.7%;
Matches 115; Conservative
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Best Local Similarity 47.0%;
Matches 151; Conservative
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                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (3294164)
JS-10-312-841-1
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SEQ ID NO 1
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Wart
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: With DNA TRANScription
TITLE OF INVENTION: With DNA TRANScription
FILE REPERENCE: 5013.1009
CURRENT APPLICATION NUMBER: US/10/240,453
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                                                            ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FRATURE:
NAME/KEY: unsure
LOCATION: (182)
US-10-240-453-259
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Pred. No. 3.4;
0; Mismatches 146; Indels
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; LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
US-10-240-453-38
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PRIOR APPLICATION WUMBER: PCT/BP01/03973
PRIOR FILING DATE: 2001-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10019173-8
PRIOR APPLICATION NUMBER: DE 10043826-1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-31
PRIOR PILING DATE: 2000-06-31
NUMBER OF SEQ ID NOS: 350
LENGTH: 17848
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 49.7%;
Matches 145; Conservative (
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45.6%;
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Best Local Similarity
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA

TITLE OF INVENTION: Transcription

TITLE OF INVENTION: Transcription

TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated

TITLE OF INVENTION: With DNA TRANSCRIPTION

FILE OF INVENTION: With DNA TRANSCRIPTION

FILE OF INVENTION: WITH DNA TRANSCRIPTION

CURRENT FILING DATE: 2002-10-02

PRIOR APPLICATION NUMBER: DE 1001-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06
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// LOCATION: (76), (90)

OTHER INFORMATION: unsure at all n locations

// OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

US-09-960-352-5785
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Pred. No. 0.78;
0; Mismatches 179;
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                                    MUSCLE AND FAT DEPOSITION
CURRENT FILING DATE: 2001.006/37-21(10298)C
CURRENT FILING DATE: 2001.09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 516
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APPLICANT: OLEK, Alexander
DPLICANT: PIEPENBROCK, Christian
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Best Local Similarity 46.2%;
Matches 154; Conservative
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ORGANISM: Bos taurus
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PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREESEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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Publication No. US20030204075A9
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Best Local Similarity 62.3%;
Matches 71; Conservative (
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GENERAL INFORMATION:
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GENERAL INFORMATION
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                            1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGAT
                                                                                                                                                                                                                                                                                                                TTTGGATTTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAAACAATAAAAGAA
                                        1088 AGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAA
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2.8%; Score 46.4; DB 15, Length
Best Local Similarity 45.6%; Pred. No. 5.5;
Matches 164; Conservative 0; Mismatches 196; Indels
Mismatches 196; Indels
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LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
10-239-676-28
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LACATION NUMBER: US/10/239,676

PRIOR APPLICATION NUMBER: PCT/EPO1/03968

DE 10019058.8

DE 10019173.8

DE 10028259.7

DE 10038259.7

PRIOR PT-
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APPLICANT: PIEPENBROCK, Christian
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ORGANISM: Artificial Sequence
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2000-04-06
Matches 164; Conservative
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EQ ID NO 28
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TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
9927 ATAAATAATAACTAAAATTAAAAAAAAAAAATATATTAACATTTTAATTTTC
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TITLE OF INVENTION: Identification and Mapping of Sing)
TITLE OF INVENTION: Polymorphisms in the Human Genome
FURE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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1325 GAAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCC 1384
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                                                                                PRIOR APPLICATION NUMBER: US 60/185,188
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APLICATION NUMBER: US 60/156,358
PRIOR APLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASLESEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 233686
LENGTH: 616
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Pred. No. 1.8;
0; Mismatches
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EQ ID NO 17272
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DATE: 2000-06-15
ATION NUMBER: US 60/216,820
DATE: 2000-07-07
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US 60/198,676
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ATE: 2000-05-25
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FILING DATE: 2000-07-25
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US 60/218,006
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lication No. US20030165831A1
ERAL INFORMATION:
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Best Local Similarity 62.3
Matches 71; Conservative
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US-10-027-632-233686
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Copyright (c) 1993 - 2004 Compugen Ltd.
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:uo ur	February	1, 2004,	21	36:50	February 1, 2004, 21:36:50 ; Search time 4063.41 Seconds (without alignments) 10782.626 Million cell updates/sec	
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2888711 segs, 20454813386 residues

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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pmmaipsnamiptvoafflipoiagpsnopollaffaaaaspssyvaavoqastmarp
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,

rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

[Dases 1 to 1071]

Lam, B., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M.,

Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H.,

Bilm, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.

Direct Submission

Submitted (17-APR-2001) DNA Sequencing and Technology Center,

Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                      901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA
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/protein_id="AAK43925.1"
/db_xref="GI:13877695"
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This clone was isolated by RT-PCR.
Location/Qualifiers
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|mol_type="mRNNA"
| Aref="Laxon:3702"
|chromosome="II"
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same, and methods of use
Patent: WO 0216655-A 1034 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)
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Matches 1071; Conservative 0; Mismatches
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GATCTAACCATCAACGGCGTCAGAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120
                                                                    GATCTAACCATCAACGGGGTCAGAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120
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ukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, Ca 4710, USA
The RENEW Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA, "RIKEN stabiologis Full-Length cDNA,"; Seki,M., Narusaka,M., Ishida,J. Satou,M., Satou,M., Sakurah,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL CDNAs: Yamada, K. Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldenith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Mu, H.C., Yamamura, Y., Yu, G., Lim, B., Cheuk, R., Jones, T., Karlin, Neumann, G., Kim, C., Lam, B., Lin, J., Miradd, M., Nguyen, M., Palin, C., L., Shini, P., Southwick, A., Davis, R.W., BCker, J.R. and Theologis, A.
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Arabidopsis thallana putative PCF2 DNA binding protein (At2g45680)
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Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, B., Dale, J.M.,
Deng, J. M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Nui, H.C., Yamamura, Y., Yu, Gi, Bowger, L.,
Carnindi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Nartisaka, M., Nguyen, M., Palm, C.J., Sakurai, T.
Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1102)
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, B., Dale, J.M.,
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, B., Ouale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Ouacch, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.
Satou, M., Seki, M., Shinni, P., Southwhork, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                           permatophyta, Magnoliophyta, eudicotyledons, core eudicots, osids; eurosids II; Brassicales; Brassicaces, Arabidopsis, osids; eurosids
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mol_type="mRNA"
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ecotype: Columbia"
                                                                                                                                                                                    Arabidopsis thaliana (thale oress)
Arabidopsis thaliana
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chromosome="2"
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                                                                                                      AY113981.1 GI:21281084
DEFINITION
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                                                                 ACCESSION
VERSION
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Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
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                                                   NLMKKKKRRRPSNSEYIDISDAVSASSGLAFIATTTTIOPPQALASSTVAQQLLPQGMY
PMWAIPSNAMIPTVGAFFLIPQIAGPSNQPQLLAFPAAAASPSSYVAAVQQASTMARP
                                                                                         PPLOVVPSSGFVSVSDVSGSNLARATSVMAPSSSSGVTTGSSSSIATTTHTTREEDED EI VEKQELHQFMSTTTARSSNH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 1180
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KDRHTKVEGRGRRIRMPATCAARIFOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120
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100.0%; Score 1071;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches
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ramada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Baris,R.W., Ecker,J.R., and Theologis,A., Shinozaki,K.,
Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY056214 11near PLN 18-SEP-2002
Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680),
mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                               961 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1020
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841 GTTGTTCCAAGCAGCGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA 900
                                                                                                                                         901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAAGCGTAACAACCGGTAGTTCATCATCGTCA 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Yamada, K., Banh, J., Balano, F., Dale, Cl. M., Goldanith, A., D., Lee, J. M., Gondera, C. S., Quach, H. L., Tarag, C. C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C. Palm, G. J. Lam, B., Lih, J. Meyers, M. C., Miranda, M., Ngryen, M., Brim, P., Southwick, A., Tracy, S. E., Davis, R. W., Ecker, J. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada, K. (SGP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA ): Sexi, W. Narusaka, M., Ishida, J., Satuch, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                               901 GOGACGTCGGTTATGGCTCCGAGCTCAAGCCTAACAACCGGTAGTTCATCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                             1021 GAGCTTCACCAGTTCATGAGCACCACAACAGGCACGGTCATCGAACCACTGA 1071
1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCAGGGTCATCGAACACACTGA 1071
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Arabidopsis thaliana
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases 1 to 91854)
11in, X., Kauli, S., Town, C.D., Bentto, M.-I., Creasy, T.-H., Haas, B.-M.,
Mu, D., Malti, R., Bowman, C.L., White, O., Nierman, W.C. and Fraser, C.M.
Arabidopsis thaliana chromosome: 2 BAC F17K2 genomic sequence
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(bases 1 to 91854)

Town,C.D. and Kaul,S.

Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, cdtown@igr.org on Apr 18, 2002 this sequence version replaced gi.6598396.

Address all correspondence to:at@tigr.org
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The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes were identified by a combination of several methods: Gene
prediction programs including Genscan+ (Chris Burge;
                                                                                                                                                    GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGATCCAACCTCCG
                                                                                                                             CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG
                                                                                                                                                                                                               TGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAA
                                                                                                                                                                                                                                                      763 TGGGCTATTCCATCAAACGCAATGATTCCGAGGTCGGAGCTTTCTTCTTGATTCCACAA
                                                                                                                                                                                                                                                                                                   ATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTTCCCGCCGCCGCTGCTTCGCCG
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Arabidopsis thalians chromosome 2 BAC F17K2 genomic sequence, complete sequence.
Ac003680

AC003680.3 GI:20197048
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A CONTRACTOR OF THE SECOND
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AC003680/c
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                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative PCF2 DNA binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRELGHKSDGETIRWLLENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTTNADSDMĞE
NLMKKKKRKRPSNSEYIDISDAVSASSGLAPIATTTTIQPPQALASSTVAQQLLPQGMY
PMWAIPSNAMIPTVGAFFLIPQIAGPSNQPQLLAFPAAAASPSSYVAAVQQASTWARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLQVVPSSGFVSVSDVSGSNĪSRATSVMAPSSSSGVTTGSSSSIATTTHTLRPFSL
EIYEKQELHQFMSTTTARSSNH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGTTGAAGGAAGAGGAAAAGGATACGGATGCCTGCCACGTGTGCGCTAGGATTTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AATCTGATGAAGAAGAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGATCCAACCTCCG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463 AACGCIGAGCCGGCGATTATAGCCGCCACGGTACGGAACGGTTCCCGCCATCGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACACG
                                                                                                                                                          /clone="RAFL07-08-P04 (R10678)"
/note="This clone is in a modified pBluescript vector
(FLC-1) as a BamH1/XhoI insert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTTCAAGACCTTTCCAAGTAAAT
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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                                                                               organism="Arabidopsismol type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                            evidence=experimental
                                                                                                    mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 g
                                                                                                                                                                                                                                      ecotype: Columbia"
                                                                                                                                                                                                                                                      l. .1660
/gene="At2g45680"
                                                                                                                                                                                                                                                                                                                     gene="At2g45680"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="At2g45680"
                                                                                                                                               chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                 .102
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Best Local Similarity
Matches 1071; Conserv
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RIGIN
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complement (join (3414. 3616,3639. 3825,3916. 3965,
4092. 4215,4582. 4712,4769. 4864,4948. 5188,5352. 5374,
5506. 5585,5670. 5980))
                                                                                                                                                                                                                                                                                                                                                                         AĞINGAKÇALIEMVILPAKRRDLFTGLRRPARVTSLLGLLLFGPPGNGKTMLAKAVAS
SEÇATFRIVSASSLTSKMIDSINGTRSTSENBERREKKEFLIQFDGYTSNPDDLVII
IGATNKPQELDDAVLRRLVKRIYVPLPDSNVRKLLFKTKLKÇPHSLSDGDIDKIVKE
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/translation="MRTMGIIDSF6SILNEESKKDPSVSSSTSSESWNGIDGVPVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFLVESEKDPENMNDKYLRDIIINFMIAGKDTTAALLSWFLYMLCKNPLVQEKIVQE
RDVTPSHEKTTDVNGFVESINEBALDEMHYLHAALSETLRLYPPVPVDMRCAENDDV
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GPRICLGKDPAYRQMKIVSMALLHFPRFKMADENSKVYYKRMLTLHVDGGLHLCAIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MGGKGKKRREKNYLAAHGGPARLPPPPDRSKQDDVPSTLRILAMN
YTSPSPHDSPTKQVVBKTBKLKKABYWVPATBEDGDBSVVEKKKKKKKKKRNGTDLARPEN
YTABIDGRSKRKEREKKYWEAKKOKKGKKGKTEDTLERNFPKHEQITRFGDVVQAPLKLA
VVPKARKSTLSASQERLRLQAIDAYRSKKGWTARPGVPIPAVMMQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MEILTSIAITVATTIFIVLCFTIYLMIRIFTGKSRNDKRYAPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSDELYDYETEIAREKPTYRFLSPGQSEILTADPRNVEHILKTRFDNYSK
ADLLGHGIFAVDGEKWRQQRKLSSFEFSTRVLRDFSCSVFRRNASKLVGF
                                                                                                                                                                                                                                                                                                                  SSEKEKVRSYREKISNWQNQVSERLQALGVGMSENKRTVAYPSSASVSSTASRYRKTI
                                                                                                                                                                                                                                                                                                                                               OKTPVARGGVATPRNPKDAAASPKPVKESGNVYDDKLVEMINTTIVDRSPSVKWDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SEFALSGKAFDAQDLLMRCTLDS1FKVGFGVELKCLDGFSKEGQEFMEAFDEGNVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSRFIDPLWKLKWPPNIGSQSKLKKSIATIDKPVYSLITTKRKELAKEQNTVVREDI
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ceres:35578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(0412. .9632)
/gene="At2g45520"
/note="synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(6429, .6950,7026. .7310,7386. .7724,7806. .8006,
1100. .8288)
gene="At2g45510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (join(<8412. .8678,8768. .8903,8987. .9120,
9288. .9356,9459. .>9632))
/gene="At2g45520"
complement (join(8553. .8678,8768. .8903,8987. .9120,
9288. .9356,9459. .9612))
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product="putative cytochrome P450"
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protein id="AAC06155.1"
db_xref="GI:2979546"
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product="expressed protein"
protein_id="AAC06154.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAC06153.1"
db_xref="G1:2979544"
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/rpt_family="(CA)n"
complement(9578. .9632)
/rpt_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822. .10798
gene="At2g45530"
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gene="At2g45530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   429. .8288
gene="At2g45510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ceres:82<u>2</u>0"
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http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GilmmerH, see Mihaela Pertea http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant http://www.tigr.org/sefilab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@figgr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/db/gli.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wushington.edu/RN/RepeatMasker (Arian Smit, http://ftp.genome.washington.edu/RN/RepeatMasker html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synony": F17K2.3; predicted by genscan"
complement(join(<3414. .3616,3639. .3825,3916. .3965,
doy2. .4215,4882. .4712,4769. .4864,4948. .5188,5352. .5374,
5506. .5585,5670. .>5980))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGGLFHGIHFSPDTVLQERGCFRLQGVETDNEPGRCRRTDGKKWRCSKDVLSGQXYCD
CHMHRGMKKKHPVDTTNSHENAGFSPLTVETAVRSVVPCKDGDDQKHSVSVWGITLPR
/SDEKSTSSCSTDTTITDTALRGEDDDEBXLSLFSPGV"
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(GGELYGVLKQNGHLTEQQAATYIASLSQALAYCHGKCVIHRDIKPENLLLDHEGRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adfgwsvossnkrktmcgtldylapemyenrdhdyavdnwtlgilcybflygnpffe
resokdtfkriikidlsfplippnvseeaknlisqllvkdpskrlsiekimohpwivkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MSKKSTESDAGNTEKQWSLADFEIGRPLGKGKFGRVYLAREAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tränslation="DESKPSVQKFFPEVSDKCLEAAKFSSNRKNDIIARSREWKNMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="overlap with BAC clone F4L23 (AC002387:1. .1281)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="synonym: F17K2.2; contains a protein kinase domain rofile (PDOC00100)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (join (<1002. .1112,1208. .1280,1366. .1580,
1655. .1750,1886. .2128,2260. .>2388))
'gene="At2g45490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omplement [join(1002. .1112,1208. .1280,1366. .1580,
655. .1750,1886. .2128,2260. .2388))
gene="At2g45490"
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vrotein_id="AAC06151.1"
b_xref="G1:2979542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Arabidopsis thaliana"
mol type="genomic DNA"
cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="hypothetical protein"
protein id="AAF18607.2"
db_xref="G1:20197053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="synonym: F17K2.27"
oin(<57. .242,335. :>747)
gene="At2g45480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(57. .242,335. .747)
gene="At2g45480"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db xref="taxon:3702"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="F17K2"
complement(1. .1281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="At2g45480"
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05	RESULT 6 BT008779 LICOUS: BT008779 BT008779 BEFINITION Arabidopsis thaliana At5g51910 mRNA, complete cds, AccEssion BT008779 VERSION VERSION FILCONA, FILCONA, FILCONA, ACCESSION BT008779 (G1:31711723) KEYMONDS FILCONA, BT008779 (G1:31711723) KEYMONDS FILCONA, BT008779 (G1:31711723) KEYMONDS FILCONA, BT008779 (G1:31711723) KEYMONDS FILCONA, BT008779 (G1:31711723)	NISM NCE ORS	KATILIN HOLMARIA, SAWAI, Lam, S Pallm, C Maranda, M Nguyen, M. Onodera, C. S., Pallm, C. J., Uach, H.L Sakurai, T. Satou, M., Seki, M. Southwick, A., Toriumi, M Wong, C Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R. W., Theologis, A. TITLE Arabidopsis ORF clones JOURNAL Unpublished REFERENCE 2 [Dases: 1 to 882]	- 1	COUNTIL SUBMITTED 113-1019. SAIK INSTITUTE GENOMICS MELECTED SAIM INSTITUTE GENOMICS COUNTILE SAIM INSTITUTE GENOMICS SAIM INSTITUTE FOR BIOLOGICAL STUDIES, 10010 N. Torrey Pines Road, La Jolla, CA 920. USA COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of FARL CDNAS (RAFL CDNA SAIO) SAIO, M., Kamitya, A., Sakurai, T., Carrinci, P., Kawai, J., Hayanizaki, Y. and Shinozaki, K. Carrinci, P., Kawai, J., Andahizaki, Y. and Shinozaki, K.	The Salk, Stanford, PGEC (SSP) Consortium members constructed an sequenced the pUNI (ORF) clones using the RAIL CDNAS: Kin. J., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J. Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K. Yu, G., Davis, W., Theologis, A., and Ecker, J. R.
/db_xref="G1:2979545" /translation="MGSSSSGGDDLEKQQQQQXDKSPQKQSESANESNHLTIVVCN /translation="MGSSSSGGDDLEKQQQQQXDKSPQKQSESANESNHLTIVVCN GDSSREELVGQIPPEKEVGLSRNGSSHEQCRVCLQDKEFVLIELGCQCRGGLAKARRS CIDAWFRIKGSNQCICTQVVAVNVTPPETQPTNVWWRIDPSYRQERERGCFSPLW VARAVQREANNFSNIAYPPAL" WHRAVQREANNFSNIAYPPAL" Gene // All 100 09	ATGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 60	121 CCCACAGTGASTCTCGAGCCGAGGCGGTGATGCCGTTTTCAATGTCTTTA 180		y 361 AACGCTGAGCCGATTATAGCCGCCACGGGAACGGTACCGCCATCCCCCATG 420 b 74771 AACGCTGAGCCGCGATTATAGCCGCCACGGGTACGGAACGGTTCCCGCCATGCTAGCTA	181 AATCTGATGAAGAAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC 540	601 CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 660 74531 CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 74472 9 661 TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGGATTTCTTCTTGATTCCACAA 720 9 74471 TGGGCTATTCCATCAAACGCAATGATTACTGACGGTCGTGGAGCTTTCTTCTTTTTTTT

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Best Local Similarity 75.9
Matches 195; Conservative
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FVDVNDSCHSSVTSGLAPITASNYGVNILAVVTQGFVPFWFMGMGTAFVTGGPDQMGQ
MMAIPTVATAPPLLNVGARPVSSYVSNASDAEAEMSTSGGGTTQPLRDFSLEIXDKREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o mRNA linear PLN 06 DEC 2002
mRNA for unknown protein, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GACTAAACCGGCTCCGAAGAGACCGACTTCTAAAGACCGTCACACGAAAGTAGAAGGACG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 AGGTCGGAGGATCCGAATGCCGGCGGTTGCGCTCGCGTCGTTTCAATTGACCCGTGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AGGGAGAAGGATACGGATGCCTGCCACGTGCGGCTAGGATTTTTCAATTAACTCGAGA
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               Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakaijima, M., Enju, A., Kamiya, A., Narusaka, M., Carninoi, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Arabidopsis thaliana full-length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          PVKTKPAPKRPTSKDRHTKVEGRGRRIRMPAGCAARVFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.7%; Score 157.8; DB 8; 75.9%; Pred. No. 1.4e-36;
                                                                                              'organism="Arabidopsis thaliana"
mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                   51
                                                                                                                                                                                                   'note="This clone is in pUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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> xref="GI:31711724"
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2 (bases 1 to 1046)
                                                                                                                                                                                                                                                                   note="unknown protein"
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Arabidopsis thaliana At5g51910 r
this work. Shing... contributed equally to this ... Location/Qualifiers
                                                                                                                                                                                                                                                                                                           product="At5g51910"
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1. .882
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                                                                                                                                                                                  clone="U60996"
                                                                                                                                                              chromosome="5"
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Best Local Similarity 75.9
Matches 195; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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JOURNAL
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AUTHORS
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AK118579
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                                                         FEATURES
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Direct Submission

Submission

Submission

Submission

Submissed (35-70072002) Motoaki Seki, RIKEN Genomic Sciences

Center; 1-7-22 Suehiro-cho, Teurumi-lu, Yokohama, Kanagawa
230-0045, Japan (8-mail:mseki@gso.riken.go.jp, Tel:81-45-503-9625)

Fax:81-45-503-9586)

An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) plant J. 15707-703,
Seki et al. (2002) Science 296:141-1459. CDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.

This clone is in a modified pluestript vector.

Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for

further details.
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pvytypapyrptskdrhtkyegrgrrirmfaggaarvrqitrelghysdgetirwlis
raepalibatgfgyvpalavsvngtlkiptsspylndggrdgdglikkrrkkngtsd
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MMAIPTVATAPFLNVGARPVSSYVSNASDAEABMETSGGGTTOPLRDFGLIYDKREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 AGGICGGAGGATCCGAATGCCGGGGGTTGCGCTCGTGCTCGGGTTTCAATTGACCGTGA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 GACTAAACCGGCTCCGAAGAGACCGACTTCTAAAGACGGTCACAGGAAAGTAGAAGGACG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 ACTIGGICACAAAICCGACGGAGAAACGAIACGGIGGIIATIGGAACGAGCIGAACCGGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATTATAGCCGCCACGGGTACGGGTTCCCGCCATCGCCATGTCGCTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GATAATITGAAGCAACCGGAACTGIACCGGCCCATIGCTGTATCGGTTAACGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 AGGGAGAAGGATACGGATGCCTGCCACGTGGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 157.8; DB 8; Length 1046; 75.9%; Pred. No. 1.4e-36; 1.75.9%; O; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY086379 mRNA linear Arabidopsis thaliana clone 247645 mRNA, complete s
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="common name: thale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="At5g51910/MJM18_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone="RAFL19-81-E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAC43179.
/db_xref="GI:26452182"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 CITAAAAATCCCGACGA 451
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TITLE

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All Submitted GUDGAPE-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-01612, Japan (E-mail:Ynakamu@kazusa.or.jp, Tel:81-438-52-3934)

Address for correspondence: Kaos@kazusa.or.jp address for correspondence: Kaos@kazusa.or.jp address for correspondence: Kaos@kazusa.or.jp address for correspondence: Asos@kazusa.or.jp address for correspondence: Japan annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MyMBS.Genes with similarity to protein in the databases are described in protein is inilarity are described as 'unknown protein.'

The software programs used to opredict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, Http://compbbio.orml.gov/grail-13/1, NetGenes (S.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brende St.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brende St.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brende St.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brende St.M. Hebsgaard, et al., CBS, Technical University of SplicePredictor (Volker Brende St.M. Hebsgaard, et al., CBS, Technical University, Mashington University Rome. Mathington University Rome. Splice (Amile Budy, Mashington University Rome) (Amis Budy, Endere may not be the entire insert of this clone is MICO24, and the after insert of this clone is MICO24, and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24 and the as clone is MICO24
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Arabidopsis thallana genomic DNA, chromosome 5, Pl clone:MJM18.
AB025623 BA000015
   378 ACTIGGICACAAAICCGACGGAGAAACGAIACGGIGGIGGITATIGGAACGAGCIGAACCGGC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tracheophyta;
                                                                                                                                           438 GATAATTGAAGCAACCGGAACCGGAACTGTACCGGCTATTGCTGTATCGGTTAACGGAAC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H.
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                                                                       375 GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATGCGCCATGTCGGTTAACGGAAC
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/product="MADS box transcription factor-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheol
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence factures of the regions of 3,076,755 bp covered by P1 and TAC clones
DNA Res. 7 (1),31-63 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="CDS is reported in Acc# AB010074
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'organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                            498 TTTAAAATCCCCACCA 514
                                                                                                                                                                                                            435 CTTAAAAATCCCGACGA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Tabata, S.
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AB025623/c
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
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VERSION
KEYWORDS
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AUTHORS
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MEDLINE
PUBMED
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AUTHORS
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Direct submission

Bullect submission

Malibu, CA 90265, USA

Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbark. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent are splice axiants; including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the cotypes and therefore cleaminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ms or Lack considered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AARVPOLTRELGHKSDGETTRWILERAEPAITEATGTGTVPAIAVSVNGTLKIPTSSP
VIDGGROBGDLMKKRRKNGYDSPVDVNDSGISSTVSGLAPPTASNYGVNILANNT
QGFVPFWPMGAGTAVTGGPDQMGQMMAIPTVATAPFLANVGAPVSSYVSNASDAEAE
METSGGGTTQPIRDFSILEIYDKRELQFLGGSGNSSPSSCHET"
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 AGGTCGGAGGATCCGAATGCCGGCGGTTGCGCTCGCTCGGGTCTTTCAATTGACCCGTGA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 GTTAGGTCACAAATCCGACGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may contain polymorphisms when compared to sequences from Col.0. Genest carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1156) ver, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and eldmann, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 GACTAAACCGGCTCCGAAGAGACCGACTTCTAAAGACCGTCACACGAAAGTAGAAGACG
                                                                                                                                                                                                     Haas, B.G., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brover, V., Troukhan, M., Alexandrov, N., Lu, Y. Asidmann, K. Full-Length cDNA from Arabidopsis thaliana Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="247645"
                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3 (6), RESEARCH0029 (2002)
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|db_xref="GI:21592496"
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product="unknown"
                                                                                                                                                                               (bases 1 to 1156)
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Best Local Simi.
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IVFSQSGRLHBYSSSQMEKIIDRYGKFSNAFYVAERPQVERYLQELKMEIDRMVKKI LEVHHRKLLGQGLDSCSVTELQEIDTQIEKSLRIVRSRKAELKADQLKKLKEKERE Inslation="MVRGKIEIKKIENVTSROVTFSKRRSGLFKKAHELSVLCDAQVA complement (654, 738)
complement (654, 738)
forduct="MADB box transcription factor-like protein"
fore="CDS is reported in Acc# AB010074"
fore di MUM18.1" complement (431, 492)
/product="MADS box transcription factor-like protein"
/noce="CDS is reported in Acc#"AB010074
/number=3 product="WADS box transcription factor-like protein" note="CDS is reported in Acc# AB010074 ene_id:MJM18.1" 'omprement vetr. .340/ 'product="MADS box transcription factor-like protein" profuct="CDS is reported in Acc# AB010074 jene_id:MJM18.1" oin(7086, .7247;7585, .7832,8043, [8262,8344. 8466) INERKRIJEEVNMHHSSKGNTEGGHRTKHSSEVETDLFIGLPVTRL" svidence=not experimental
product="WADG box transcription factor-like"
protein id="BAA97222.1" LPHIHGDKCMLHEGRNVSKGVKYVFRSDVVFA" evidence=not_experimental_ product="peroxidase" protein_id="BAA97224.1" experimental 'evidence=not_experimental codon_start=1 evidence=not_experiments protein_id="BAA97223:1" xref="GI:8809683" xref="GI:8809681 unknown protein" number=1 exon exon exon exon CDS CDS SCO

LFINSTATION="MAPSKGLIFAMIFAVLAIVKDSBAALDAHYYDGSCPAAEKIILE VRNATLYDPKVPARLLRMFFHDCFIRGCDASILLDSTRSNQAEKDGPPNISVRSFYV PPPTFNVSQLIQSFAARGLSVKDMVTLSGGHTIGFSHCSSFESRLQVFSKFHDIDPSM NYAFAQTLKKKCPRTSNRGKNAGTVLDSTSSVFDNVYYKQILSGKGVFGSDQALLGDS SYLKNHDLFTVENCLTSDESKAFVKLAESLGFTHQGSRGPAYGEAYRDNHRISYNDPY LADTLWQSGLSNLFTDIKIRRKYAVGLNPNIRFYRYSAGQHFGRHIDESADLEDGNRT YYTLLIYLSGNSTKSKSKSSSSKTNDSSSAEPLVGGETVFYGSRNSIVAEVAPVEGMA translation="MNLTNLISLNLILNPPOKPRNAKMGDNGESIKWPKIKLKSNLNV **EDAKRKLEKACPRTVSCADVIAIAARDVVTLSGGPYWSVLKGRKDGTISRANETRNL** oomplement(join(8854...9420,9536...9724,9814:::10026)) /note="gene_id:MJM18.4" tkwivetfaodokaffrefaasmyklgnfgvketgovrvntrfvn complement(join(11372. 11638/11684. 12145)))
/noce="contains similarity to cytochrome P450
gene_id:MJM18.5" evidence=not_experimental%protein_id="BAA97225.1" db xref="GI:8809684

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13136 GACTAAACCGGCTCCGAAGAGGACGACTCTAAAGACCGTCACACGAAAGGACGACG 13*077* 12956 GATAATTGAAGCAAACCGGAACTGTACCGGCTATTGCTGTATCGGTTAACGGAACC12897 13016 ACTIGGICACABAICCGACGAGABAACGAIACGGIGATATHGAACGAGCIGAACGGC 12957 Ar103304 1910 bp mRNA linear PLN 01-JUL-2002 Arabidopsis thaliana AT3g47620/F1P2_170 mRNA, complete cds. AX103304 /tränslation="Mesnhegnalgyidgyttwitledpnpktkpgmmlmkqedgyldpvrkreapkraptskortikmlig pvkrkrapkraptskortikvegrerirmagacaavyrgitrelightsdgettrwilig prafalitatorgyvalaysvygytistpsspylmdggndgbdblikkrekrengsd pvdyndschesytsgilapinasvygytilmnyrogfypfyrmamgyraptygepdygy mwaiptyatapfilwygarpyssysnasdaarmstsgagytropledbyse 315 GFTAGGTCACAAATCCGACGACGAAACCATTCGGTGATGTGGACAAACGATGAGCCGGC 374 255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA 314 375 GATTATAGCCGCCACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434 to DNA binding protein PCF1 Ouery Match Best Local Similarity 75:9%; Pred. No. 2.1e-36; Matches 195; Conservative 0; Mismatches 62; Indels 14.7%; Score 157.8; DB 8; 75.9%; Pred. No. 2.1e-36; 2744 g 5153 t /codon start=1
/evidence=not_experimental
/protein_id="BAA97226.1" similarity FLI CDNA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana EPDTSLILKWKHGFKVKINKRCSS" 12896 TTTAAAATCCCGACGA 12880 complement (12395 /note="contains gene_id:MJM18.6" 435 CTTAAAAATCCCGACGA 451 AY103304.1 GI:21655288 a 2906 c 5400 AY103304 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM BASE COUNT ORIGIN CDS RESULT 10 ð 8 ð 원 엄 g ð 셤 엄 ਨੇ

Splus; electrical of the splus Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis. Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.
Kawai, J., Lam, B., Lee, J.M., Lin, Mirranda, M., Narusaka, M.,
Nguyen, M., Onodera, C.S., Palm, C.J., Onach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Mu, H.C., ., Chen, H., Cheuk, R., Meyers, M.C., Shinn, P., Banh, J., Carninci, P., Chang, R., Dale, J.M., Goldsmith, A.D. amada,K., Yamamura,Y., Yu. heologis,A. and Ecker,J.R. rabidopsis ORF clones to 1470) Cim, C.J REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

us-09-938-842a-1034.rge

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AVVAAKKPPLKRASTKDRHTKVDGRGRRIRBALCAARVFQLTRELGHKSDGBTIEWL
LOOAEPSVIAATGTGTIPANFTSLNISLRSSGSSMSLPSHFRSAASTFSPNNIFSPAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOQQQQQQRGGGVGFHHPHLQGRAPTSSLFPGIDNFTPTTSFLNFHNPTKQBGDQDSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSSGLHFMNFAAPMAFLTGQQQLATTSNHEINEDSNNNEGGRSDGGGDHHNTQRHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim, C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="mokptssilnvimdggdsvggggddhhrhlhhhrpfpppgl
gkhdpddnhoooppspsssslfslhohoolsosopsosoksopottokellotoess
                             Direct Submission
Submitted (11-M7-2002) Salk Institute Genomic Analysis Laboratory
(SIGMAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNAS : RIKEN Arabidopsis Full-Length CDNA) : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 GCCAGCTAAAAAGCCACCGTTGAAACGAGCGTCGACGAAAGAGACGACGACACGAAAGTAGA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AGGAAGAGGAAGAAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 CGGAAGAGGGAGGAGTAATAAGGATGCCGGCGTTATGTGCAGCTAGGGTTTTTCAGCTAAC. 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 TCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGCTGGTTGTTGGAGAACGCTGA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 GCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 ACCATCTGTAÁTCGCCGCCACCGGAÁCCGGÁACAATCCCGGCGAATTTCACTTCTTTAÁA 554
                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing and annotation of the RAFL CDNAs: Kim,C.J., Chen,H., Cheuk,R., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Chang,B., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu.H.C., Yamada,K., Yamada,K., Yang,C.C., Davis,R.W., Theologis,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="This clone is in pUNI 51
ecotype: Columbia"
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protein id="AAM65356.1"
db xref="G1:21655289"
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                                                                                                                                                                                                                                                                                                             Satou, M., Kamiya, A., Sakurai, T.
Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
db_xref="taxon:3702"
Theologis, A. and Ecker, J.R.
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171; Conser
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Best Local S:
Matches 171
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                             TITLE
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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, B., Meyers, M. C., Banh, J., Bowser, L., Carninci, P., Dale, J. M., Goldenth, A. D., Karlan, S. M., Sankith, A. D., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Miranda, M., Quach, H. L., Sakurai, T., Satou, M., Sett, M., Southwick, A. Tang, C.C., Torlun, M., Tomada, K., Yamanura, Y., Yu, G., Yu, S., Yu, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVVAAKKPPLKRASTKORHTKVOGRGRRIDNPALCAARVFOLTRELGHKSDGETIEWL
LOQAEDSVTAATGTOTTDANFTSLATSLRSGGSSMGLPSHFRSAASTFSPNNIFSPAM
LOOOOOOORGGGVGFHHPHLOGRAPTSSLPPGIDNPTPTTSPLNFHNPTKQEGDQDSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All Judges D. Chon, F. J. Cheuk, R., Kim, C. J., Koesema, B., Meyers, M. C., Banh, J., Bowser, L., Carninci, P., Dale, J. M., Goldsmith, A. D., Hayashitzaki, Y., Ishida, J., Jiang, P. X., Jonnes, T., Kamiya, M. Karlin-Neuman, G., Kawi, J., Liu, S. X., Miranda, M., Narusaka, M., Isuyen, M., Onodera, C.S., Palm, C. J., Pham, P. K., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Fang, C.C., Toriuni, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Arabidopsis cDNA clones
                                                                                                                                            AY058874 1755, bp mRNA linear pLN 03-NOV-2001
Arabidopsis thaliana AT3G47620/F1P2_170 mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (05-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory. The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 GTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACACGAAGGTTGA 248
                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots,
resids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
(bases I to 1755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.0%; Score 129; DB 8; Length 1755;
y 71.0%; Pred. No. 1.1e-27;
rvative 0; Mismatches 70; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thallana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="RAFL09-09-C11 (R14172) "
                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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35. .2290,2378. .2437,2672. .2734,3123. .3214,3344. .3440,
16. .4032,4174. .4392,4519. .4659,4737. .4904,5138. .5322,
91. .5584,5671. .5759,5842. .6067,6228. .6302,6413: .6526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATF1P2 101154 bp DNA linear PLN 30-NOV-1999 Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ranelation="MHIKEICLEGFKSYATRTVVPGFDPHFNAITGLNGSGKSNILDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILSMLEBAAGTRMYENKKEAALKTLEKKQTKVDEINKLLEKDILPALEKLRREKSQYM
JWANGNAELDRLKR FCVAPEYVQAEKIRDNSIHVVEEMKIKWTGIDEQTDKTQGEISE
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249 AGGAAGAGGAAGAAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAAC 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission.

Submitted (3-0NOV-1999) MIPS, at the Max-Planck-Institut fuer

Studented (3-0NOY-1999) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Kloyferspitz 18a, D-82152 Martinsried, FRG, E-mail:

lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Marcel Salannoubat and Francis Quetier, Groupement

d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue

Gaston, Cremieux, BP191, 91006 Evry Cedex, Prance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choisne, N., Robert, C., Brottier, P., Wincker, P., Cattolico, L., Artiguenave, F., Saurin, W., Weissenbach, J., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis:
                                                                                                                                                       474 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA
                                                                                                                                                                                                                                                                   534 ACCATCTGTAATCGCCGCCACCGGAACCAACCGACGGCGGAATTTCACTTCTTTAAA
                                                414 CGGAAGAGGAGGAGAATAAGGATGCCGGCTTATGTGCAGCTAGGGTTTTTCAGGTAAC
                                                                                                                                                                                                                369 GCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCCGCCATCGCCATGTCGGTTAA
                                                                                                      309 TCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGA
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mol_type="genomic DNA"
variety="Columbia"
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BU Arabidopsis sequencing, project.
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ATF1P2
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AUTHORS
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LEKQIKALTQAREASMGGEVKALSDKVDSLSNEVTRELSKLTNMEDTLQGEEKNAEKY
                                                                                                                                                                         FRAHQKSISETEANIKELQPLQTKFTDMKAQLELKNYDMSLFLKRAEQNEHHKLGDAV
KKLEEEVEEMRSQIKEKEGLYKSCADTVSTLEKSIKDHDKNREGRLKDLEKNIKTIKA
                                                                                                                                                                                                                                                        DA I OKDHDOSLSELKLI I HAKMKE CDTO I SGSTAEQEKCLOKI SDMKLDRKKLENEVTR
MEMBHKN CSVKVDKLVEKHTM I SEKRLFGNGGTDYDFESRDPHKAREELERLOTDOS
                                                                                                                                                                                                                                                                                                                                                     algiliatilekdariyildevdaaldishtonigrmikshpphsorivvsikegmps
nadviprtkpudgustvortytkos"
                                                                                                                                                   CKTTDAAKEVAFNREIRTPSVTLEGDVFQPSGLLTGGSRKGGGDLLRQLHDLAEAETK
                                                                                                                                                                                                                               QASSKDLKGHENVRERLVMEQEAVTQEGSYLKSQLTSLRTQISTLASDVGNQRAKV
                                                                                                                                                                                                                                                                                                            EKRVNKKVTAMFEKAEDEYNALMTKKNIIBTDKSKIKKVIEBLDEKKKETLKVTWV
                                                                                                                             INKI QSHLVPPRVQQATVGKGNAELALSLVGYSEELKNAMEYVFGSTF
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ene="F1P2.10"
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|ene="F1P2.10"
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Jene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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Tene="F1P2.10"
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jene="F1P2.10"
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Jene="F1P2.10"
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jene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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72786 GCGAGAGCTAGGTCATAAATCCGACGGGGGGAATAGAGTGGCTTCTTCAACAAGCTGA 72845
                                                                                                                                             72666 GGCAGCTAAAAAGCCACCGTTGAAACGAGCGTCGACGAAAGACCGACACACGAAAGTAGA 72725
                                                                                                                                                                                                                    72846 ACCATCTGTAATCGCCGCACCGGAACCGGAACAATCCCGGCGAATTTCACTTCTTAAA 72905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MR a defective suppressor mutator transposon. J denotes a sequence derived from the 3'end of the transposon. E denotes a sequence derived from the 5'end of the transposon BESRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX322174 451 bp DNA linear STS 10-JUN-2003 Arabidopsis thaliana transposon insertion STS SM_3.35210, sequence tagged site.
                                                                                                                                                                                   308
                                                                                                             248
                                                                                                                                                                                                                                                                                                                               369 GCCGGCGATTATAGCCGCCACGGGTACGGAACGGTTCCCGCCATCGCCATGTCGGTTAA 428
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukarayophyra, Viridiplantae, Streptophyta; Embryophyra; Tracheophyta;
Spermatophyra, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                             GICTICGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACCAAGGTTGA
                                                                                                                                                                                   249 AGGAAGAGGAGAAGGATACGGATGCCTGCCACGTGCGGCTAGGATTTTTCAATTAAC
                                                                          Gaps
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                                    cch 12.0%; Score 129; DB 8; Length 101154; al Similarity 71.0%; Pred. No. 1.9e-27; 171; Conservative 0; Mismatches 70; Indels 0;
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/varlety="Columbia-0 NASC stock code N1092"
db_xref="taxon:3702"

    .451
    /organism="Arabidopsis thaliana"

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139 c 87 g 83 t
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73.1%;
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   homolog"
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Unpublished
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Best Local Similarity
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PROTEIN 4 PRECURSOR (LHCI TYPEIII CAB-4) - Arabidopsis
thaliana, SWISSPROT:CB24_ARATH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product = "CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR
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5585. .5670
/gene="F1P2.10"
3441. .3915
/gene="F1P2.10"
/number=10
3916. .4032
/gene="F1P2.10"
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/gene="F1P2.10"
/number=13
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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Jene="F1P2.10"
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gene="F1P2.10"
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jene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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RESULT 14 AY081706 LOCUS

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1 (bases 1 to 1440).
Cheuk, R., Chen, H., Kim, C.J., Koesma, B., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.W., Goldsmith, A.D., Hayashizaki, Y., Bahida, J., Jiang, P. X., Ones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.K., Miranda, M., Quach, H.L., Saturai, T., Satur, Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Arabidopsis cDNA clones
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRPKNESHSSSSSSQLLDHNOMGNYLVQSTAGSLPTSQSPATAPFWSSGDNTQNLWA
FNINPHHSGVVAGDVYNPNSGGSGGGSGVHLMNFAAPIALFSGQPLASGYGGGGGGG
EHSHYGVLAALNAAYRPVAETGNHNNNQONRDGDHHNNHQEDGSTSHHS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'translation="MDPDPDHNHRPNFPLQLLDSSTSSSTSLAIISTTSBPNSEPKK
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VIAATGTGTIPANFTSLNISLRSSRSSLSAAHLRTTPSSYYFHSPHQSMTHHLQHQHQ
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Pred. No. 2.2e-26;
0; Mismatches 999
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ed equally to this work as PIS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          'product="At1g69690/T6C23_11"
'protein_id="AAL87359.1"
'db_xref="G1:19547991"
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Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                   'note="unknown protein"
'codon start=1
                                                                                                    organism="Arabidopsis"
                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
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(bases 1 to 978)
Chenk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninoi, P., Chang, E., Dale, J.W., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Miranda, M., Narusaka, M., Nguyen, M., Southwick, A., Tang, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A.
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Arabidopsis thaliana At1g69690/T6C23_11 mRNA, complete cds.
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                      59; Indels
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Unpublished
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                      Matches 160; Conservative
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and Ecker, J.R.
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TITLE JOURNAL

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)

TITLE

COMMENT

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2 (bases 1 to 1440)
Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Boker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Repersty M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Chodera, C.S., Palm, C.J., Paman, P.K., Vamann, H.L., Southwick, A., Tang, C.C., Tortumi, M., Yamada, K., Yamannra, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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|db xref="GI:15912213"
|translation="MDPDPDHNHRPNFPLQLLDSSTSSSSTSLAIISTTSEPNSEPKK
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VIAATGTGTIPANFTSLNISLRSSRSSLSAAHLKTTPSSYYFHSPHOSMTHHLQHQHQ
VRPKNESHSSSSSSSQLLDHWQMGNYLVQSTAGSLFTSQSPATAPFWSSGDNTQNLWA
                                                                                                                                                                                                                                                                                                                                                              Submitted (10-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNINPHAGVVAGDVYNPNSGSGGGSGVHLMNPAAFIALFSGQPLASGYGGGGGGG
BHSHYGVLAALNAAYRPVAETGNHNNNQQNRDGDHHHNHQBDGSTSHHS"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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stress condition to which a plant cell has been exposed plants with increased tolerance to these abiotic stresses Identifying a and producing

Claim 144; SEQ ID NO 1034; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an arbaidopsis thaliana stress regulated gene (ABZ12196-ABZ1754) used in methods of the invantion.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by

Sequence 1071 BP; 287 A; 288 C; 256 G; 240 T; 0 other;

Gaps · . DB 24; Length 1071; 0; Indels Mismatches Score 1071; Pred. No. 0; .. 100.0%; Query Match
Best Local Similarity 100.
Matches 1071, Conservative

9 1 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 1 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAAGGCAAAGATCAAACTCTAAGAGCCGTT

121 CCCACAGTGAGTCTCGAGGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 180 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACACG 240 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGGCTTCGACTAAAGACCGTCACACG 240

AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGGCCATCGCCATG 420 301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360

CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 660 TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCT 661

961 ATTGCAACAACGACGCACACGCTGAGAACTTCTCCCTAGAGATATACGAGAAACAA 1020 TCGTCTTACGTCGCCGCTGTTCACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAA.840 900 661 IGGGCIATICCATCAAAGGCAATGATTCCGACGGTCGGAGCTTTCTTCTTCATCCACAA 720 901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 960 841 GITGITCGAAGCAGCGCTTTGTATCCGTTTCAAACGTTAGCGGTTCGAATTTATCAAGA 721 Arcecrecrescencearcascereasurarerascereceses GTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTTATCAAGA GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAA 881 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCAGGGTCATCGAACCACTGA 1071 1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCAGGTCATCGAACCACTGA 1071 841 781 781 901 721 ર્જ B 8 B P

ABX61156 standard; DNA; 460 BP ABX61156; RESULT 2 ABX61156/c

Arabidopsis thaliana polynucleotide #502

(first entry)

26-FEB-2003

Thale cress; gene; ds; genetic manipulation; plant; blosynthesis; genetic modification; environmental stress; disease resistance; fungicide; insecticide; stress tolerance.

Arabidopsis thaliana. US2002142319-A1.

03-OCT-2002.

13-AUG-1999; 99US-148784P. 11-AUG-2000; 2000US-0638258: 07-AUG-2001; 2001US-0924035

HAMILTON C M. PRICE J. L. HARGISS I R. MATHEW A V. RAMEAKA J G GORLACH J. HARG/) PAGE/) MATH/) BBBBBBBBBBKBKBKBKBKCKKKKKCKAKCCKAKCK

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Haas WD; An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y, Page A, Mathew AV, Ledford BL, Woessner JP, Hi An Y, Gorlach J, Rameaka JG, Garcia CA;

WPI; 2003-102509/09.

Novel Arabidopsis thaliana nucleic acid useful

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transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes
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Claim 1; Page 158; 277pp; English.

The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that medulate the expression or function of the polypeptides, for mapping functional regions of the protein, in diagnosis, for studying associated physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or biosynthetic products in plants and to create genetically modified and transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as it fungicides and insecticides, and for identifying factors involved in plants, occurred to incorrete in plants, or and for identifying factors involved in plants of insertable to instruments. biosynthetic pathways of nutritional, commercial or medici. Sequences ABX60655-ABX61554 represent Arabidopsis thaliana polymucleotides of the invention

Sequence 460 BP; 113 A; 103 C; 134 G; 109 T; 1 other;

ij DB 25; Length 460; 1; Indels Query Match
41.8%; Score 448; DB 25
Best Local Similarity 99.6%; Pred. No. 5e-134;
Matches 459; Conservative 0; Mismatches 009

659 460 GCAAGCTCTGGCATCATCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 401 GCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTGTGCCGCAAGGAATGTATCCGAT

719 GTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCT 099

AGTIGITCCAAGCAGCGCTTIGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAG 899 GTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCTTTACA GTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACA 281 780 840

222

959

42

ABL93850 standard; cDNA; 453

.BL93850/c ESULT 3

ABL93850

(first entry) 10-JUN-2002

Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis; Arabidopsis thaliana nucleic acid sequence Ref:2027615 SEQ ID NO:615

26-JAN-2001; 2001US-0770444. genetic modification; gene; 27-JAN-2000; 2000US-178502P Arabidopsis thaliana. HAMILTON C M. LEDFORD B L. WOESSNER J.P. RAMEAKA J G. RAINES T M. MATHEW A V. GORLACH J. DAVIS K R. ALLEN K. HURBAN P. US2002023280-A1. HOFFMAN SLATER PAGE 21-FEB-2002 (ALLE/) (HOFF/) (HURB/) RAME/) PAGE/) MATH/) GORL/) WOES/) HAAS/)
GARC/) RAIN/) SLAT/)
DAVI/) YYYY/ LEDF/)

Haas WD; Ur, naab Hoffman N; Ledford BL, Woessner JP, H Davis KR, Allen K, Hoffma Price JL, Ledford BL Gorlach J, An Y, Hamilton CM, P. Rameaka JG, Page A, Mathew AV, Garcia CA, Kricker M, Slater T, Hurban P, WPI; 2002-267486/31.

New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein -

Claim 1; SEQ ID 615; 44pp; English.

comprising a sequence capable of hybridising under stringent conditions to a sequence (S1) selected from any one of the 999 sequences given in AB193235 to AB194344 (1). have insecticide and tungicide activities, and they can be used as protein expression modulate proteins of the proteins of their encoded proteins that modulate the expression of function of their encoded proteins, mapping physiclogical pathways (1) can also be used (1) for the genetic marphulation of cells patricularly plant cells; (2) in screening assays of various plant strains to determine the strains that a best capable of withstanding a particular disease or environmental stress; (3) for enhancing or inhibiting production of a biosynthetic product in a plant; anagenic organisms. C form part of the printed format directly from the The present invention describes an Arabidopsis thaliana nucleic acid (I) acids, to generate ribozymes or antisense oligonucleotides, and as single-stranded DNA probes or as triple-stand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms. (4) as probes in mapping and in diagnosis, in genetic modification and for screening purposes, to generate additional copies of the nucleic for this patent did no btained in electronic Note: The sequence data for this specification, but was obtained

Sequence 453 BP, 111 A; 100 C, 132 G, 107 T; 3 other,

Score 439; DB 24; Length 453; Pred. No. 4e-131; 0; Mismatches 41.0%; nilarity 99.1%; Conservative 0 Similarity Query Match Best Local Simil Matches 450;

Gape

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9909-0132485.
9908-0132863.
9908-0132863.
9908-0132863.
9908-0134219.
9908-0134219.
9908-013421.
9908-0134341.
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 CTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATGTGGGGCT
                                                                                                 ATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAAATCGCT
                                                                                                                                                                                                     TACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAAGTTGTT
                                                                                                                                                                                                                                                                                                     CCAAGCAGCGGCTTTGTATCCGTTTCAGAGGTTAGCGGTTCGAATTTTATCAAGAGCGACG
                                                                                                                                                                                                                                                                                                                                       TCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCAATTGCA
                                creecarcarccacrerectacacracacracaccacaagaareraccaarcaagacr
                                                                     CTTGATTCCACAAATCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 25210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCAGTICATGAGCACCACAACAGCACGGTCAT 1060
                                                                   ATTCCATCAAACGCAATGATTCCGACGGTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCAGTTCATGAGCACCACAACAGCACGGTCAT
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99US-0130891.
99US-0131449.
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                                                                                                                                                                                                                                                                     CCAAGCAGCGGCTT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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PR 22-JUL-1999, 9908-0145087,
PR 22-JUL-1999, 9908-0145186,
PR 23-JUL-1999, 9908-0145186,
PR 23-JUL-1999, 9908-0145186,
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PR 13-AUG-1999, 9908-0149323,
PR 23-AUG-1999, 9908-01551030,
PR 13-AUG-1999, 9908-01
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258 GACTABACCGGCTCCGAAGAGACCGACTTCTAAAGACCGTCACACGAAAGTAGAAGACG 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 Addreda Addreda Ariecede de George de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Control de Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 1156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.9%; Pred. No. 4.9e-40;
Matches 195; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis cDNA encoding a transcription factor #85
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PILGRIM M.
CREELMAN R.
DUBELL A J.
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99US-0160814
99US-0160815
99US-0160981
99US-0160981
99US-0161404
99US-0161405
99US-0161405
99US-0161359
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99US-0161350
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16-NOV-2000, 2000US-0713994.
16-APR-2001, 2001US-0837944.
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                                                                  - OCT - 1999;
- OCT - 1999;
- OCT - 1999;
- OCT - 1999;
- OCT - 1999;
- OCT - 1999;
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(PILG/)
(CREE/)
(DUBE/)
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ABK65233
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ABK65217 standard; cDNA; 1231 BP

RESULT 6 ABK65217

ABK65217;

Keddie J; Pineda O;

Jiang C, Yu G, 1

J, Heard J, J Riechmann JL,

Dubell AJ,

4, Creelman R, Dubell A Ratcliff O, Reuber JL,

Pilgrim M,

Adam L,

RATCLIFF O. REUBER J L. RIECHMANN J :

(RATC/) (REUB/) (RIEC/)

PDAM

ADAM/

(JIAN/

HEARD J

PINEDA O.

(YUGG/)

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The invention relates to 1 of 232 isolated or recombinant polymucleotiques canding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polymucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered benetype as compared to a wild-type or reference plant, or the plant as compared to a wild-type or reference plant, or the plant exhibits accepted secondarial as compared to a wild plant. Also included are a transgenic plant trait as compared to a wild plant. Also included are a transgenic plant trait as compared to a wild plant. Also included are a transgenic plant trait as compared to a wild plant. Also included are a transgenic plant trait sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant caquences comprising inputting sequence information selected from one of 46% fully defined sequences given in the specification. The isolated or recombinant polymucleotide is used for producing a plant having a neodified trait, the method comprising selecting a polymucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the corour into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait (e.g. increased the modified trait (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth are, lasf and flower senescence and many other traits listed in the recording the present sequence is one of the 232 polymucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600 accarcrerarcecceccaccesarcesarcesarcecesesarrreacricrinaa 659
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                                                                                                       An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 TCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 GTCTTCGACAGGACCACCATTGAAGAGGCTTCGACTAAAGACCGTCACGAAGGTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGCTAAAAAGCCACCGTTGAAACGAGCGTCGACGAAAGACGGACACACGAAAGTAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 1728 BP; 526 A; 414 C; 362 G; 426 T; 0 other;
                                                                                                                                                                                                          Claim 4; Page 373-376; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.0%;
Matches 171; Conservative
WPI; 2002-292022/33.
P-PSDB; AAU93047.
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The Intention Fenaues to 1 of 25 isolated to 1 counciling in Fenaues to 1 complements, fragments, or related polynucleotide with 31% to 95% complements, fragments, or related polynucleotide with 31% to 95% complements, fragments, or related polynucleotide with 31% to 95% compared to a wild-type or plant exhibits an altered trait as compared to a wild-type or reference plant, or the plant exhibits enterpoly compared to a wild-type or reference plant, or the plant exhibits enterpoly compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequence from a database comprising a plurality of known plant sequence from a database comprising a plurality of known plant compliant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encombinant polynucleotide or an antisense mucleic acid, inserting the polynucleotide or an antisense mucleic acid, inserting the polynucleotide or an antisense mucleic acid, inserting the polynucleotide or an antisense mucleic acid, inserting the polynucleotide or an antisense mucleic acid, inserting the polynucleotide or an event or a cell of a plant to overexpress introducing the vector into a plant or a cell of a plant to overexpress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 1 of 232 isolated or recombinant polynucleotides
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plant -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keddie J;
Pineda O;
                                                                                                       Plant, ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
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Yu G,
                                                                      Arabidopsis cDNA encoding a transcription factor #69.
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Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 315-317; 941pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coducing the vector into a plant or polypeptide or antisense nucleic
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Ratcliff O, Reuber JL, I
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P-PSDB; AAU93031.
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DUBELL A J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAM L.
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Adam L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAACCTTAAAA 441
plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower sensecence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                        Score 124.6; DB 24; Length 1231;
Pred. No. 2.7e-29;
0; Mismatches 99; Indels 0;
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                                                                                                                                                                                                                                                                                              Sequence 1231 BP; 323 A; 317 C; 230 G; 361 T; 0 other;
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Best Local Similarity 65.0%;
Matches 184; Conservative (
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R 23-UIL-1999; 99US-01493.

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R 23-UIL-1999; 99US-01493.

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R 23-UIL-1999; 99US-01493.

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R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-01493.

R 23-UIL-1999; 99US-0
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298 CCTCCTCCTAAAGGACCTCTACTAAGACCGACAACAAAAGTCGAAGGCCGAGGCCGT.357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 GCCGCCACGGGAACGGGAACGCTTCCCGCCATGTCGGTTAAACGGAACCTTAAAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 CACAAATCCGACGACGAAACGATTCGGTGGTTGTTGGAGAAACGCTGAGCCGGCGATTATA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 gecelenkagagakerdakkenrickagerakerrekerrerrakkenterekerregr 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin-dependent protein kinase; CDK; CDC2a; CDC2b; VbDBP; cell cycle; DNA binding protein; interacting protein; environmental stress; growth regulator; herbicide; nematode resistance; plant breeding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 CGGATCCGTATGCCTGCCATGTGTGTGTGTGTTTTCAGCTCACACGTGAGCTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.0%; Pred. No. 2.8e-29;
Matches 184; Conservative 0; Mismatches 99; Indels 0;
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1..957
/*tags a
/*product= cdc2b-interacting_protein
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                   99US - 0160768 . 99US - 0160770 . 99US - 0160815 . 99US - 0160815 . 99US - 0160981 . 99US - 0161405 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 016135 . 99US - 0161392 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 90US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 0161393 . 99US - 01613
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99US-0160767
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                   21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
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29-OCT-1999
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AAA51413
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Mon Feb

stress tolerance; fungicide screening; insecticide screening

Gossypium hirsutum

gene; da.

JS2002040490-A1.

04-APR-2002

26-JAN-2001; 2001US-0770423 7-JAN-2000; 2000US-178512P

HAMILTON C M.

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GORLACH J.

AMEAKA J G RAINES T M.

> YUYY/ RAME/

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PAGE/)

Arabidopsis thaliana expressed sequence related polynucleotide #332. ABX62217 standard; DNA; 422 25-FEB-2003 ABX62217; ESULT 9 BX62217 ≿ બ્ર

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CDC2a and CDC2b are the only CDK genes to have been characterized in detail in Arabidopsis thaliana. They were used as bait in a two-hybrid screening assay with a cDM, library of a plant cell suspension as prey. The plant cell cycle interacting proteins identified were designated colds. From the plant cell cycle interacting proteins identified were designated buy115, PHO90-like protein, Vb33 Vb89, VbDAHP and VbHSF. The nucleic colds, vectors comprising them, the proteins they express, antibodies that bind to them and or inhibitors of their protein expression and/or activity may be used for modulating the cell cycle in an animal or plant, cycle proteins in a plant or animal cell, as positive or negative regulators of cell proliferation for modifying the growth inhibition caused by environmental stress conditions, eggeven of plants in normal or suboptimal nutrient conditions, especially property or cell prosphorus), for use in a screening method for inhibitors or activators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The VbDBP clone is very similar to the A. thaliana putative DNA binding protein and also contains a lot of homologies with Oryza sativa PCF2. VbDBP interacts with cyclin-dependent protein kinase (CDK) CDC2b but not
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                                                                                                                                                                                                                                                              Nucleic acids encoding plant cell cycle interacting proteins, useful for regulating plant growth and in recombinant DNA protocols
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     Inze D;
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Torres Acosta JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 131-132; 152pp; English.
De Veylder L, Boudolf VKCK,
                                                                                                        WPI; 2000-431601/37.
                                                                                                                                                            P-PSDB; AAY96818
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232 AAGAGAAGCTCTAACAAAGACAGACACACTAAAGTCGAAGGTCGAGGGTCGACGAATTCGG 291
                                                                                                                                                                                                                                                                                                                                                                                  GACGCCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCACG 390
                                                                                                                                                                                                                                                                                                                       292 ATGCCTGCTCTTTGTGCTGCTAGGATTTTTCAATTGACTAGAGAATTGGGTCATAAATCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                             352 GATGGTGAAACTATCCAGTGGCTGCTTCAACAAGCTGAGCCATCGATTATTGCAGCTACT 411
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                                                                                                                                   Gaps
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0
      11.0%; Score 118; DB 21; Length 1081; larity 73.3%; Pred. No. 3.4e-27; Conservative 0; Mismatches 55; Indels 0;
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Query Match
Best Local Similarity
Matches 151, Conserve
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Transgenic plant; plant; genetically modified cell; environmental stress; ribozyme creation; disease resistance;

(first entry)

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The invention describes an Arabidopsis thaliana nucleic acid (I). The polypeptide (II) encoded by (I), transganic plant (III) or genetically modified cell (IV) are useful for screening "candidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or producing compositions that modulate the expression or function of its encoded protein, for mapping functional regions of the protein, in encoded protein, for studying associated physiological pathways, for genetic manipulation of calls, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding production of biosynthetic product fina plant, for withstanding production of biosynthetic product fina plant, for producing polypeptides, as probes for the detection of mancing or inhibiting production of biosynthetic product in a plant, for samples, to generate additional copies of (I), to generate ribozymes or oligonucleotides, as single stranded DNN probes or as triple-strand for transport of correct genetically and such as the correct genetically and such as the correct of correct control of the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as the correct genetically and such as and such as the correct genetically and such as the correct genetically and such as the correct genetic
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anhanced tolerance to environmental stress, or to produce a factor. This
sequence represents a nucleic acid that may correspond to naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             occurring Arabidopsis thaliana expressed sequences. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic organisms, such as plant cells and plants. (II) or (III) is useful for introducing or improving disease resistance and stress
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Davis KR, Allen K, Hoffman N;
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Rameaka JG, Page A, Mathew AV,
Garcia CA, Kricker M, Slater T,
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KRICKER M
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ALLEN K.
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                                                                                                                                                                                                                                                                                                                                                                         187 CCGATGGTCAAACCATAGAGTGGCTTCTCCGTCAAGCTGAGCCTTCTATCATAGCGGCCA
specification, but was obtained in electronic format directly from the
US patent office at
                                                                                                                                                                                               67 TTAAGAAACCACCGTCTAAAGATCGACACAGCAAAGTTGACGGAAGAAGAGAAGAAGAGATTC
                                                                                                                                                                                                                                                                                                   127 GTATGCCAATCATTTGCGCAGCTCCAGTTTTTCAATTGACCAGAGAGTTAGGTCACAAGT
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Pineda O;
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                                                                                                                           DB 25; Length 422;
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                                                                                                                       Score 111.2; DB 25; Length
Pred. No. 3.3e-25;
0; Mismatches 58; Indels
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Ratcliff O, Reuber JL, Riechmann JL, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis cDNA encoding a transcription factor #67
                                                                                       Sequence 422 BP; 111 A; 100 C; 118 G; 93 T; 0 other;
                                  US patent office at
segdata.uspto.gov/sequence.html?DociD=999909770423.
                                                                                                                                                                                                                                                                                                                                                                                                            389 CGGGTACGGGAACGGTTCCCGCCA 412
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Best Local Similarity 71.6%;
Matches 146; Conservative
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2001US-0837944.
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CREELMAN R.
DUBELL A J.
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P-PSDB; AAU93029.
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PINEDA O.
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16-APR-2001;
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controlled as compared to a wild type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant tatit as compared to a wild plant. Also included care a transgenic plant trait as compared to a wild plant. Also included readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant equences comprising inputting sequence information selected from one of 46 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polympeptide or antisense nucleic acid, thereby producing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth cate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides
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                                                                                                                              The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
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                   An isolated or recombinant polynucleotide used to produce a transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 GTATGCCAATCATTTGCGCAGCTCGAGTTTTTCAATTGACCAGAGAGTTAGGTCACAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.4%; Score 111.2; DB 24; Length 1009; Best Local Similarity 71.6%; Pred. No. 5.2e-25; Matches 146; Conservative 0; Mismatches 58; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 4718.
                                                                                       Claim 4; Page 309-310; 941pp; English.
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Best Local Similarity
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KEDD/
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es 58; Indels
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ID ABK65353 standard; cDNA; 1172
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29-OCT-1999
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An isolated or recombinant polynucleotide used to produce a transgenic
microbial disease resistance, herbicide resistance, seed yield;
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Pred. No. 2.3e-21;
0; Mismatches 65; Indels 0
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Ratcliff O, Reuber JL, Riechmann JL, Yu G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding an A. thaliana transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 845-846; 941pp; English
                                                                                                                                                                                                     MENDEL BIOTECHNOLOGY INC.
              fruit yield; growth rate; leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.1%;
Matches 139; Conservative
                                                                                                                                               22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
                                                                                                                     22-AUG-2001; 2001WO-US26189
                                        Arabidopsis thaliana
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P-PSDB; AAU93167.
                                                                                                                                                                                                                              CREELMAN R. DUBELL A J.
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                                                                                                                                                                                                                                                                                                               RATCLIFF O
                                                                                                                                                                                                                                                                                                                                                                   PINEDA O.
                                                                                                                                                                                                                                                         HEARD J.
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                                                                                                                                                                                                                                                                                                  ADAM L.
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Adam L, Ra
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The invention relates to 1 of 232 isolated or recombinant polymucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polymucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared
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312 cadarodocadacadricaniderracirogrodacoadecorrorariandocoada 371
                                                                                                                                 252 GTATGCCGATTATATGTGCTGCTCGTGTTTTTCAGCTAACGAGAGAGCTTGGTCATAAGT 311
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plant -
                                        192 TGAAGAAACCACCGGCGAAAGATCGACATAGCAAAGTCGATGGAAGAGGGGAGAAAATCC
                                                                                    GGATGCCTGCCACGTGTGCGCCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keddie J;
Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
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Yu G, 1
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Ratcliff O, Reuber JL, Riechmann JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 312-314; 941pp; English.
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16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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REUBER J L.
RIECHMANN J I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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CREELMAN R.
DUBELL A J.
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PINEDA O.
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P-PSDB; AAU93030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2002
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Adam L, Ra
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209
                                                                                    269
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REUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILG/)
CREE/)
DUBE/)
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                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
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phenotype as compared to a wild-type or reference plant, or the plant exhibits ecropic expression or altered expression or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polymucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequence given in the specification. The isolated or recombinant polymucleotide is used for producing a plant having a modified trait, the method comprising selecting a plant having a modified trait, the method comprising selecting a plant having a polympotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a caid into an expression vector, introducing the vector into a plant or a caid into an expression of plant or a selecting or a modified trait (e.g. increased producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, seed and finit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A. thaliana transcription factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 cccacaacaacaacaaacaacaacaacaacacacacaacaacaacaacaacaa 180
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9.2%; Score 98.6; DB 24; Length 1263;
Best Local Similarity 55.4%; Pred. No. 6.9e-21;
Matches 191; Conservative 0; Mismatches 154; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 AGCCAGCTATCATCGCAGCCACCGGAACTGGAACCATACCGGCGA 465
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PR 08-UUL-1999; 99UG-0142803.

PR 12-UUL-1999; 99UG-0142803.

PR 13-UUL-1999; 99UG-0142812.

PR 13-UUL-1999; 99UG-0143542.

PR 15-UUL-1999; 99UG-0144005.

PR 15-UUL-1999; 99UG-0144005.

PR 15-UUL-1999; 99UG-0144013.

PR 19-UUL-1999; 99UG-014432.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014433.

PR 20-UUL-1999; 99UG-014463.

PR 21-UUL-1999; 99UG-014463.

PR 22-UUL-1999; 99UG-014463.

PR 22-UUL-1999; 99UG-014463.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

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PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 22-UUL-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

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PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01450.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

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PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

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PR 23-UUC-1999; 99UG-01490.

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PR 23-UUC-1999; 99UG-01490.

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PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99UG-01490.

PR 23-UUC-1999; 99U

16-NOV-2001; 2001WO-US43101 16-NOV-2000; 2000US-249222P

WO200240688-A2 23-MAY-2002 Walker EL, Dellaporta WPI; 2002-490144/52. P-PSDB; ABB83920.

(UYYA) UNIV YALE

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DB 21; Length 1379;
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                                                                                                                                                                                                                                                                                 8.7%; Score 93.2; D
68.8%; Pred. No. 4e-1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   GGATGCCTGCCACGTGTGCGGCTAGGATTT
9US-0157753
                                                                                                                                                                                                                                                         99US-0161993
                                                                                                                                                                                                                                                                                                 Conservative
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99US-01
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99US-01
99US-01
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Best Local Simi:
Matches 128; (
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The invention relates to an isolated nucleic acid molecule (1), maize yellow stripe 1 (ys1) or yellow stripe1-like (ys1) from Arabidopsis (ABN85763.ABN85771). (I) is useful for generating transgenic plants which metal or heavy metal contaminate from soil and for bioremediation of metal or heavy metal contaminated soil. (I) may also be used to aler the distribution of iron within the plant body so that edible parts of crop plants brave more iron. Transgenic plants may also be used in conventional plant breeding schemes to produce progeny which also contain the gene of interest. The present sequence is that of the Arabidopsis ysl encoding cDNA of the invention.

New yellow stripel and yellow stripel-like genes, useful for altering the distribution of iron within the plant body so that edible parts of crop plants have more iron, or for producing plants useful in enhancing iron uptake from soil

Claim 1; Page 114-159; 187pp; English

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388
                                               268
                                                                                       254
                                                                                                                                   328
                                                                                                                                                                                                                                                                  CAGATGGCCAAACAATTGAATGGTTACTTCGTCAAGCAGAGCCTTCTATTATAGCTGCAA 374
                                            195 TGAAGAACCACCGGAAAGATCGACATAGCAAAGTCGATGGAAGAGGGGAGAAGAATCC
                                                                                                                                   ITCAATTAACTCGAGAGTTAGGTCACAAAT
                                                                                                                                                                                GTATGCCGATTATATGTGCTGCTCGTGTTTTTCAGCTAACGAGAGGTTGGTCATAAGT
                                                                                                                                                                                                                          CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA
  Gaps
  ö
58;
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Maize, transgenic, plant, yellow stripel-like, yel; Arabidopsis, iron uptake, bioremediation; yellow stripe 1; yel; gene; ss.

Arabidopsis sp

Arabidopsis yellow stripel-like 4 encoding cDNA SEQ ID NO 9

(first entry)

21-OCT-2002

ABN85767;

ABN85767 standard; cDNA; 83698 BP.

Search completed: February 1, 2004, 21:58:51 Job time : 322.739 secs

18740 18741 Grinocricocriciscascaassarriarcaarraassarraassarrassarrassarra 18801 adandendadacneringaandehinderinciaeridehdekteandeanaenentendinde 18860 210 GAAGAGGATTCGACTAAAGACCGTCACACGAAGGTTGAAGGAAAGAGGAGAAGGATACG 270 GAIGCCIGCCACGIGIGGGGTAGGAITTTTCAATTAACTCGAGAGTTAGGTCACAAATC 330 CGACGGCGAAACGATTCGGTGGTTGTTGGAGAAACGCTGAGCCGGCGATTATAGCCGCCAC Sequence 83698 BP; 26295 A; 15150 C; 15104 G; 27149 T; 0 other; ö Score 89; DB 24; Length 83698; Pred. No. 8.3e-17; 0; Mismatches 70; Indels 0 18861 TGTAATGGTATCAAACCCAC 18881 390 GGGTACGGGAACGGTTCCCGC 410 8.3**%**; Best Local Similarity 65.2 Matches 131; Conservative Query Match Best Local 셤 8 ద ઠે 셤 ઠે ઠે

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US-08-232-463-14
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Sequence 14, Appl
                                                                                                                               (without alignments)
6701,220 Million cell updates/sec
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Sequence 12199,
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                                                                                                              February 1, 2004, 21:45:16; Search time 70.5426 Seconds
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Sequence 57
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Sequence 6,
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| /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
| /cgn2 6/ptodata/2/ina/6A_COMB.seg:*
| /cgn2 6/ptodata/2/ina/6A_COMB.seg:*
| /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
| /cgn2 6/ptodata/2/ina/PdTUS_COMB.seg:*
| /cgn2 6/ptodata/2/ina/PdTUS_COMB.seg:*
| /cgn2 6/ptodata/2/ina/PdTUS_COMB.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
US-09-252-99IA-8192
US-09-252-99IA-8112
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US-09-621-5120-546
US-08-621-517-195
US-07-982-712-1
US-08-125-619-3
US-08-145-5280-1
US-08-998-416-436
US-09-98-416-436
US-09-773-816-1
US-09-773-816-1
US-09-774-918-7
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery
Score Match Length DB ID
                                                                                                                                                                                         US-09-938-842A-1034
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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18 2172
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1553
2396
23673
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Perfect score:
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                                                                                                                                                                                                                               Sequence:
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                                                                                                                Run on:
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	28	29.8	2.8	2628	4	US-09-294-531B-5	Sequence 5, Appli
	29		2.8	4062	4	US-09-620-312D-348	Sequence 348, App
	30	29.8	2.8		Н	US-08-759-444-2	N
	c 31	29.8	6.8		m	US-08-680-897-1	Sequence 1, Appli
	32	29.8	2.8	38155	4	US-09-453-702B-79	7
	33	29.8	2.8	4403765	٣	US-09-103-840A-2	7
	m		2.8	4411529	m	US-09-103-840A-1	Sequence 1, Appli
	L.)		2.8	1302	N	US-08-529-600D-3	ď
	36		2.8		~	US-08-973-275-6	9
	m		2,8	-1	m	US-09-122-632-3	Sequence 3, Appli
	38		2.8	4065	4	US-09-016-434-1105	110
	6		2.8		m	US-08-685-871-1	Sequence 1, Appli
	0 40		.8	3196	4	US-09-453-702B-11	Sequence 11, Appl
	c 41	29.4	2,7		4	US-09-313-294A-5277	Sequence 5277, Ap
	c 42	29.4	2.7		m	US-09-007-005-17	Sequence 17, Appl
	c 43	29.4	2.7		m	US-09-244-796-17	17,
	44	29.4	2.7	N	Н	US-08-676-967-2	2,
	45	29.4	2.7	2277	Н	US-08-676-974-2	Sequence 2, Appli
						ALIGNMENTS	
ps.	RESULT	'n					

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US-08-22-463-14

US-08-22-463-14

Bequence 14, Application US/08232463

Facent No. 5670367

CENERAL INPORMATION:
APPLICANT: PARKER, F.
APPLICANT: PALKER, F. G.
TITLE OF INVENTION:
RECOMBINANT POWLED.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKER, F. G.
TITLE OF INVENTION:
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKER, F. G.
TITLE OF INVENTION:
APPLICANT: BACKERS:
ADDRESSE: FOLGY & Lardner
STATE: UA
COUNTIER NEADABLE FORM:
MEDIUM TYPE: PLOSY/MS-DOS
COUNTIER NEADABLE FORM:
MEDIUM TYPE: PLOSY/MS-DOS
COUNTIER IN BACKER: US/08/232/463

COUNTIER IN BACKER: US/08/232/463

FILING DATE: DALENTION DATA:
APPLICATION NUMBER: US/07/935,313

FILING DATE: 28-AGG-1931
ATTORNEY APPLICATION NUMBER: 28-AGG-1931
ATTORNEY INFORMATION:
PLILING DATE: SC-AGG-1931
ATTORNEY SCEPTION NUMBER: 29-768

REGISTRATION NUMBER: 29-768

FILING DATE: CANANTHON:
FILING DATE: SC-AGG-1931
ATTORNEY SCEPTION NUMBER: 29-768

FILING DATE: SCEPTION NUMBER: 30472/114 INMO
TELEFRONE: (703) 633-4109
TELEFRONE: (703) 633-4109
TELEFRONE: (703) 633-4109
TELEFRONE: (703) 633-6-9300
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TTELEFRONE: (703) 632-9300
TTELEFRONE: (703) 632
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y Match 4.1%; Score 44; DB 1; Length 7218;

IMMEDIATE SOURCE:

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542 CCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGATGCAACCTCCGC 601
                                                                                                                                           661
                                                                                                                                                                                                                                                                                                                782 CGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAAG 841
                                                                                                                                                                                                               GGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAAA 721
                                                                                                                                602 AAGCICIGGCAICAICCACIGIGGCICAGCAACTICIGCCGCAAGGAAIGIATCCGAIGI
                                                                                                                                                                                                                                                                                        TCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGGCGGCCGCTGCTTCGCCGT
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGITCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTAT 895
                            .
Best Local Similarity 2.3%; Pred. No. 0.0011;
Matches 8; Conservative 203; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: STAINNER, F. G.
APPLICANT: FLAKNER, F. G.
NUMBER OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1800 Diagonal Road, Suite 500.
CITY: Alexandria
STATE: VB.
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PROMPTER: PROMPTER: POSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: EP 91 114 300.
FILING DATE: 26-ANG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PULDATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30. TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAN. 999149
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FUNTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nuclei
STRANDEDNESS:
TOPOLOGY: li
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APPLICANT: MACC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELER REFERENCE: 107196.136
CURRENT PELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
RIOR PRING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                     255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA 314
                                                                                                                                                                                                                                                                                                                                                                                     GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 CTTAAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAAAATCTGATGAAGAA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 CCAAGTAAATCCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 CCAAGCTGGAACAGCTGGAGGCCTATAGCAGACGACGCCACCGGAGAGGCCCTGAGCACC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AATGTCTTTAGCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGA 230
                                                                                                                                                                                                                                                                                                       315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 GAAACGTAAAACGACCTTCTAACAGTGAGTATATAGACATAAAGCGACGCCGTTTCAGCTTC
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (291)
, OTHER INFORMATION: Identity of nucleotide at the above locations are US-09-252-991A-8192
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0
                                                                  Length 7218;
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49.2%; Pred. No. 2.1;
tive 0; Mismatches 90; Indels
                                                                                                         Indele
                                                              Query Match
3.8%; Score 41; DB 1; Les
Best Local Similarity 2.2%; Pred. No. 0.01;
Matches 8; Conservative 205; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8192, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.2
Matches 87; Conservative
, CLONE: PTZGPt-Fls
US-08-232-463-14
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US-09-252-991A-8192
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3941480 CTGGCGGACAAAGCGCCCCGGGGGTGCTGGCGGGCCCGCCGCCGATAACCCCACCGGCA 3941539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1136 AYCCNTTYCCNMGNGTNTTYWSNGCNTGYWSNMGNMGNCARYTNMGNGCNTTYTYMGNA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 TNTGYGGNAAYGGNTTYGTNGARGCNGGNGARGARTGYGAYTGYGGNCCNGGNCARGART 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637 CTGCCGCAAGGAATGTATCCGATGTGGGCTATTCCATCAAACGCAATGATTCCGACGGTC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 GGAGCTITCTICATTCCACAAATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      817 ATGGCTAGACCACCTCCTTTACAAGTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGAC 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    877 GTTAGGGGTTCGAATTTATCAAGAGGGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGC 936
                                                                                                                                                                                                 133 CTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTCAATGTCTTTAGCTCCACCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1196 ARGGNGGNGGNTGYYTNWSNAAYGCNCCNGAYCCNGGNYTNCCNGTNCCNGCNY
                                                                                                                                             Gapa
                                                                                      DB 3; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2406;
                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.0%; Score 32.2; DB 4; Length 2
Best Local Similarity 25.2%; Pred. No. 4.1;
Matches 82; Conservative 47; Mismatches 197; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAMMALIAN ADHESION PROTEASE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                            3941540 redecederacedecederareacedecederacede 3941571
                                                                                                                                                                                                                                                                                                        193 TCGACAGGACCACCATTGAAGAGAGCTTCGAC 224
                                                                                   Score 32.8; DE Pred. No. 68; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Nand
TITULE APPLICANT: BISHOP, PAUL D.
FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
CURRENT FILING DATE: 2000-08-02
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1316 GYMGNGAYYTNTGYTGYTTYGCNCAY 1341
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     ) OTHER INFORMATION: represent a, t, c
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(2406)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-632-098-5
    Sequence 5, Application US/09632098
    Patent No. 6420154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                   Query Match 3.1%;
Best Local Similarity 59.8%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
LENGTH: 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .09-632-098-6
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                                                                                                                                                                                                                                   Sequence 8112, Application US/09252991A
SATURENT NO. 6551795.

JENERAL INFORMATION:
MARC J. RUBENTIEL OF INVENTION:
MITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PILE OF INVENTION:
PILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (2266)
CTHER INFORMATION: Identity of nuclectide at the above locations are unknown.
JS-09-252-991A-8112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 AATGTCTTTAGCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 CCAAGTAAATCCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTC 170
130 AATACCGGCACCCGCATCGCCGATAACCAGAACACCCTGAAGGCCGGCGAGCGCGGACCG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
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                                                                                                          190 redrigeredakokericarekidededakakokiekeekerredakekekedede 246
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
IITLE OF INVENTION: TUBERCULOSIS
TILE REFERENCE: 24366-20007.00
                                                      Score 33; DB 4; Length 2874;
Pred. No. 2.5;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 812
LENGTH: 2874
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.2%;
Matches 87; Conservative
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                     09-252-991A-8112/c
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Query Match
Best Local Simil
Matches 53; C
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US-08-961-083-111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637 CTGCCGCAAGGAATGTATCCGATGTGGGCTATTCCATCAAACGCAATGATTCCGACGGTC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 GGAGCTITCTICTICATICCACAAAICGCIGGICCGTCGAAICAGCCICAGIIATIAGCI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 TITCCCGCCGCCGCTGCTTCGCCGTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACG 816
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: TUBERCHICOSIS
TITLE OF INVENTION: TUBERCHICOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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          APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Nand
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                              SEQ ID NOS: 26
FastSEQ for Windows Version 3.0
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COTHER INFORMATION: H37Rv
US-09-103-840A-1
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stent No. 6294328
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US-09-632-098-6
                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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SENGTH: 4411529
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LENGTH: 2439
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3947108 GCGGACAAGGCGGCGCGGGGGGTGCTGGCGGGGCCCGGCGCGCATAACCCCCACCGGCATCG 3947167
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                                      Gaps
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TITLE OF INTENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human General
DB 3; Length 4411529;
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                                      Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
OPERATING SYSTEM: MSDOS version 6.2
                                    36;
                                                                                                                                                                                                 3947168 GCGGCACCGCGCGCGCGCCGCCCCCGC 3947196
Score 31.4; D
Pred. No. 95;
0; Mismatches
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                                                                                                                                                        196 ACAGGACCACCATTGAAGAGAGCTTCGAC 224
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                  Sequence 111, Application US/08961083
Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pplication US/09536784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Brookes, A. Ander REGISTRATION NUMBER: 36
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
               Similarity 59.6
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Matches 63; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Choi e
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Patent No. 65730
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Sequence 195, Application US/08961527
Patent No. 6420135
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REGISTRATION NUMBER: 36,373
Drmanac, Radoje T
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                          FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: HP Vect
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..
US-09-620-312D-546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798 TGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAAGTTGTTCCAAGCAGCGG 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Choi et. al.
WENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      858 CITIGIAICCGITICAGACGIIAGCGGIICGAAITIAICAAGAGCGACGICGGIIAI 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                      TITLE OF INVENTION: Streptococcus pneumonia
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 30.6; Di
53.8%; Pred. No. 5.5;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
FLASSIFICATION: CURNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 111: IS-09-536-784-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MICHELLE S. MATKE
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB.
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e 546, Application US/09620312D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO. 111;
SEQUENCE CHARACTERISTICS:
LENGTH: 412 base pairs
                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 53.8
Matches 63; Conservative
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GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 ATAGGTCGCCACCTCTTTTGCCCTCCACGATGTTCTTCAGAGTCCTGTGCATCAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAAACTCTAAAGAGCCGTTGATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Indels
: No. 6569662el Nucleic Acids and : Polypeptides
                                                                       CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
FRIOR APPLICATION NUMBER: 09/552,317
FRIOR PILING DATE: 2000-04-25
FRIOR PRILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Dt. FL_Genes Version 1.0
SOFTWARE: Dt. FL_Genes Version 1.0
LENGTH: 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.9%; Score 30.6; D
Best Local Similarity 55.0%; Pred. No. 9.9;
Matches 60; Conservative 0; Mismatches
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/961,527
FILING DAIE:
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821 AGAACTICGACGCAGCTICCGCGGCTCCGCCCAGGCAICGAGGCAGCATCAGGAGCC 880
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US-08-545-528D-1/c
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SEQ ID NO 3
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/07982712
Patent No. 5436391
GENERAL INFORMATION:
APPLICANT: Hidday FUJIMOTO, Kimiko ITOH
APPLICANT: Mikihiro YAMAMOTO, and KO SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Producti
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700
CITY: Washington
STREET: N.M., #700
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                                                           DB 4; Length 6693;
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                                                                                              54; Indels
                                                           Score 30.6; DB
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 30.4; Di
54.5%; Pred. No. 15;
tive 0; Mismatches
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HOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                     Query Match
Best Local Similarity 53.8%;
Matches 63; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pairs
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IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warren M. Cheek,
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19921127
CLASSIFICATION: 800
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Best Local Similarity
Matches 61; Conserva
; TOPOLOGY: linear
US-08-961-527-195
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STATE: D.C
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                                                                                                                                                                                                                                                                                                                              US-07-982-712-1
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880 AGCGGTTCGAATTTATCAAGAGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTA 939

Conservative

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GENERAL INFORMATION:
APPLICANT: Fraser et al.
TILLE CANT: Fraser et al.
TILLE CANT: Fraser et al.
TILLE CANT: Fraser et al.
TILLE CANT: Fraser et al.
Patent No. 633773
TILLE CANT: Thereof, and Uses Thereof
FILE REFERENCE: PB193P1
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/483,018
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR PILING DATE: 1995-06-07
NUMBER OF SED ID NOS: 1
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 CCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAACGATCCAACCTCCGC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
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                                               881 cecaccreardeacarcreaacadearcacarcracracaceaceacacad 932
940 ACAACCGGTAGTTCATCGTCAATTGCAACAACAACGACGCACACGCTGAGAG 991
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: BARBOUK, ALAN G.
APPLICANT: WEINSTOCK, GLONGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 7766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
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                                                                                                                                                                              pplication US/09125619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                    JERRILYN K.
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Best Local Similarity 48.5.
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US-08-545-528D-1
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ö Query Match 2.8%; Score 30.4; DB 4; Length 580073; Best Local Similarity 47.0%; Pred. No. 2.1e+02; Matches 94; Conservative 0; Mismatches 106; Indels 0; Gaps

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3282 AAATACTTTTTTTTTGACGAAAAACTCAAACTTTAAAGAAGAAGTAAGGGGGATTAAGA 3223

1051 GCACGGTCATCGAACCACTG 1070

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Search completed: February 2, 2004, 03:00:11 Job time : 101.543 secs

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Sequence 615, App
Sequence 257, App
                                                                                                                                                                  (without alignments)
9695.297 Million cell updates/sec
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                                                                                                                                         February 1, 2004, 21:42:55 ; Search time 402.599 Seconds
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Cgn2_6/ptodata/2019_mbna/US07_PUBCONB.seq:*
| Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PEGCONB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBCONB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCONB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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| Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-938-842A-1034
US-09-924-035A-502
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US-10-225-068-165
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Gapop 10.0 , Gapext 1.0
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10-278	10-26	09-934	፵	0	-09-878-	10-26	10-26	10-26	US-10-260	9-770	US-10-242-05	8-781	US-10-027	US-10-02	9-864	US-10-156	10-128	-10-1	10-18	10-18	10-198-	10-02	10-02	10-32	10-32	10-26	-3	09-887	10-26	5
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Reps, Joe1
APPLICANT: Reps, Joe1
APPLICANT: APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227, 866
FRIOR APPLICATION NUMBER: US 60/227, 866
FRIOR PELLING DATE: 2001-08-24
FRIOR PELLING DATE: 2001-06-24
FRIOR FILING DATE: 2001-06-22
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches
Sequence 1034, Application US/09938842A Patent No. US20020160378A1
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121 CCCACAGTGAGTCTCGAGCC	181 GCTCCACCGTCTTCGACAGC	241 AAGGTTGAAGGAAGAGGAC 	301 CAATTAACTCGAGAGTTAGG	361 AACGCTGAGCCGGCGATTAT	421 TCGGTTAACGGAACCTTAAA 	481 AATCTGATGAAGAAGAAAGAAGAAGGAAGGAAGGAAGGAA	541 GCGTTTCAGCTTCCTCGG	601 CAAGCTCTGGCATCATCCAC	661 TGGGCTATTCCATCAACGC	721 ATGGTGGTCGTCGTCGAATCA	781 TCGTCTTACGTCGCCGCTGI	841 GTTGTTCCAAGCAGCGGCTT	901 GCGACGTCGGTTATGGCTCC	961 ATTGCAACAACAACGACGCA	1021 GAGCTTCACCAGTTCATGAG
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Sequence 1034, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel

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APPLICANT: ZIL., TONG
TITLE OF INVENTION: STRESS-RECULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938;842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR PRILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100:0%; Score 1071; DB 12; Length 1071; Best Local Similarity 100:0%; Pred. No. 0; Matches 1071; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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960 AATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAAACA 1019
                                  900 AGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACAGCGGTAGTTCATCGTC 959
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393 ATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAAATCGCT 334
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41.0%; Score 439; DB 9; Length 453;
Best Local Similarity 99.1%; Pred. No. 1.1e-141;
Matches 450; Conservative 0; Mismatches 3; Indels
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APPLICANT: Garcia, Carlos A.
APPLICANT: Kricker Maja
APPLICANT: Daids. Ted
APPLICANT: Daids. Ted
APPLICANT: Daids. Keith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Lhailas Gequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LAMIANIA
FILE REFERENCE: 2027 (PARA-016 PR)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT PILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 615
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 615, Application US/09770444
Patent No. US2002023280Al
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Rameaka, Joshua G.
Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woesner, Jeffrey, P.
Haas, William David
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NAME/KEY: misc_feature
LOCATION: (1)...(453)
OTHER INFORMATION: n = A,T,C or G
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PLICANT: Gorlach, Jorn
PLICANT: An, Yong-Quan
PLICANT: Hamilton, Carol M.
PLICANT: Price, Jennifer L.
PLICANT: Raines, Tracy M.
                                                                                                                                                                                                                   1020 AGAGCTTCACCAGTI
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Best Local Similarity 99.6%; Pred. No. 8e-145;
Matches 459; Conservative 0; Mismatches 1; Indels
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NAME/KEY: misc feature
LOCATION: (1)...(460)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Arabidopsis thaliana
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121 TGATGCCGFCGTTTTCAATGTCTTTAGCTCCACCGTCTTCGACAGGACCACCATTGAAGA 180
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Pred: No. 2.4e-33;
0; Mismatches 70;
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FILE REFERENCE: MBI-0025
CUTRENT APPLICATION NUMBER: US/09/934,
CUTRENT FILING DATE: 2001-08-22
PHIOR APPLICATION NUMBER: 60/227439
PRIOR PILING DATE: 2000-08-22
PRIOR PELICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR PILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                Application US/09934455
D. US20030121070A1
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SEQ ID NO 169
LENGTH: 1728
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Best Local Similarity 71.0%,
Matches 171, Conservative
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Ineda, Omair
                                                                               215 GAGCT 219
                                                                                                                                                              181 GAGCT 185
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                                                                                                                  CGAATTTATCAAGAGCGACG 906
                                                                                                                                                                                             214 CCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGAGCGACG 155
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ITLE OF INVENTION: Expressed Sequences of Arabidopsis
ITLE OF INVENTION: thaliana
ILLE REFERENCE: 2031US (PARA-020PRV)
PERENT FILLICATION NUMBER: US/09/770,696
JERENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCAGTICATGAGCACCACAACAGCACGGTCAT 1060
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
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0010044940A1
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; ORGANISM: Arabidopeis thaliana
US-09-770-696-257
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ameaka, Joshua G
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|ford, Brooke L
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Hamilton, Carol N
Price, Jennifer I
Raines, Tracy M.
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Best Local Similarity 100.0
Matches 185; Conservative
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ENGTH: 185
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2.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AGGAAGAGGAGATACGGATGCCTGCCACGTGTGCGGCTAGGAT
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TLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
TLE OF INVENTION: POLYPEPTIDES IN PLANTS
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llarity 71.0%; Pred. No. 2.4e
Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
IEQ ID NO 165
LENGTH: 1728
                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 514442002040
CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/11,468
PRIOR FILING DATE: 2002-06-14
                                                                   APPLICANT: Mendel Biotechnology, Inc.
Sequence 165, Application US/10225068
Publication No. US20030217383A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09934455
. US20030121070A1
                                                                                                                                    Heard, Jacqueline E
Jiang, Cai-Zhong
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                                                                                                                                                                             Adam, Luc J.
Dubell, Arnold T.
Ratcliffe, Oliver
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APPLICANT: Creelman, Robert
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Yu, Guo-Liang
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LOCATION: (106)...(1575)
IS-10-225-068-165
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Best Local Similarity
Matches 171; Conserva
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299 cogarccoraroccroccarororocrocacororriroaccroacacoroada 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 GCCGCCACGGGTACGGGAACGGTTCCCGCCATGCCCATGTCGGTTAACGGAACCTTAAAA 441
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APPLICANT: RUDELT, Lynner APPLICANT: Ruder, Lynner APPLICANT: Richmann, Jose Luis APPLICANT: Richmann, Jose Luis APPLICANT: Ry, Guo-Linaing APPLICANT: Yu, Guo-Linaing APPLICANT: Pineda, Omaira TITLE OF INVENTION: Genes for Modifying Plant Traits IV FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2000-08-22
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: Parentin version 3.1
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.6%; Score 124.6; DB 11; Length
Best Local Similarity 65.0%; Pred. No. 6.5e-32;
Matches 184; Conservative 0; Mismatches 99; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10302267
o. US20030229915A1
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CRGANISM: Arabidopsis thaliana
FEATURE:
MANE/KEY: CDS
LOCATION: (107)..(1084)
COTHER INFORMATION: G805
US-09-934-455-137
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Fromm, Michael
Heard, Jacqueline
Riechmann, Jose Luis
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suber, Lynne
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u, Guo-Liang
iang, Cai-Zho
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Pilgrim, Marsl
Creelman, Rob
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APPLICANT: Broun, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
FILE REPERENCE: 51444202040
CURRENT APPLICATION NUMBER: US/10/25,068
CURRENT FILING DATE: 2002-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2002-6-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FASLESC for Windows Version 4.0
SEQ ID NO 245
LENGTH: 1231
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Pred. No. 6.5
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CANT: Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In 11.6%;
Similarity 65.0%;
84; Conservative
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u, Guo-Liang
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Reuber, Lynne
Jiang, Cai-Zhong
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Broun, Pierre
      Yu, Guo-Liang
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, LOCATION: (107)...(1084)
US-10-225-068-245
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hang, James
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Best Local Simi
Matches 184; (
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CURRENT FILING
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Pred. No. 6.5e-32;
0; Mismatches 99;
                             CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR PLING DATE: 1099-02-17
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/12,037
PRIOR APPLICATION NUMBER: 60/12,037
PRIOR APPLICATION NUMBER: 60/124,778
PRIOR FILING DATE: 1999-03-11
PRIOR PLILNG DATE: 1999-03-11
PRIOR PLILNG DATE: 1999-04-15
PRIOR PLILNG DATE: 1999-04-15
PRIOR PLILNG DATE: 1999-04-15
PRIOR PLILNG DATE: 1999-04-15
PRIOR PLILNG DATE: 1999-04-15
PRIOR PLILNG DATE: 1999-07-15
PRIOR PLILNG DATE: 1999-07-15
INVENTION: PLANT GENE SEQUENCES II
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                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/162,656
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 218
SOFTWARE: Patentin Ver. 2,1
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Heard, Jacqueline E.
Jiang, Cal Zhong
Adam, Luc J.
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 65.0%;
Matches 184; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS

) LOCATION: (107)..(1081)

; OTHER INFORMATION: G805

US-10-302-267-61
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LENGTH: 1231
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                                                                                                                                           Gaps
DB 13; Length 1231;
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                                                                         Indels
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PASTERQ for Windows Version 4.0
ESCO ID NO 675
LENGTH: 490
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CURRENT APPLICATION NUMBER: US/09/770,961
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5. US20030121070A1
                                                                                                                                                                                       TYPE: DNA

ORGANISM: Arabidopsis thaliana
FERTURE:
NAME/KEY: misc_feature
1. CCATION: (1) ... (490)
US-09-770-961-675
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Pilgrim, Marsha
Ratcliffe, Oliver
Ruber, Lynne
Riechmann, Jose Luis
Yu, Guo-Liang
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NAME/KEY: CDS
LOCATION: (27)..(746)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.4%; Score 121.6; DB 15; Length Best Local Similarity 64.6%; Pred. No. 8.5e-31; Matches 181; Conservative 0; Mismatches 99; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 GTGTTTCGTTACGAAGTAGTGGATCGACTCTCTCTGCTCC 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLICANT: Davis, Keith R.
PLICANT: Allen, Keith R.
PLICANT: Hoffman, Neil
PLICANT: Hubban, Patrick
PLE OF INVENTION: Expressed Sequences of Arabidopsis
PLE OF INVENTION: thalana
                                                       PRIOR APPLICATION NUMBER: 60/103,512
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/108,734
PRIOR APPLICATION NUMBER: 60/113,409
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver: 2.0
SETWARE: Patentin Ver: 2.0
                                               NG DATE: 1998-09-22
ICATION NUMBER: 60/103,312
                      60/101,349
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. US20030115639A1
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                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Matthew, Abraham V
Ledford, Brooke L.
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ameaka, Joshua G
FILING DATE: 1999-09-13
                                             998-09-2
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LOCATION: (143)..(1345);
OTHER INFORMATION: G802
JS-10-295-403-147
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249 AAGAGAAGCTCTAACAAAGACAGACACACTAAAGTCGAAGGTAGAGGTCGACGAATTCGG 308
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                                                                                                                                                                                                                                                                                              309 AIGCCTGCTCTTTGTGCTGCTAGGATTTTTCAATTGACTAGAGAATTGGGTCATAAATCT 368
                                                                                                                                                                                                                                                                                                                                                      331 GACGCCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCACG 390
                                                                                                                                                                                                                                                                                                                                                                                                          369 GATGGTGAAACTATCCAGTGGCTGCTTCAACAAGCTGAGCCATCGATTATTGCAGCTACT 428
                                                          Gaps
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   Length 490;
                                                       55; Indels
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Query Match
Best Local Similarity 73.3%; Pred. No. 7.2e-30;
Matches 151; Conservative 0; Mismatches 55;
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/22439
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SSOTUMARE: Patentin version 3.1
LENGTH: 1009
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163 GTATGCCAATCATTTGCGCAGCTCGAGTTTTTCAATTGACCAGAGAGTTAGGTCACAAGAGT. 222
                                                                                  329 CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA 388
                                                                                                                                  223 CCGATGGTCAAACCATAGAGTGGCTTCTCCGTCAAGCTGAGCCTTCTATCATAGCCGCCA 282
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Pred. No. 2.7e-27;
0; Mismatches 58; Indels 0;
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TITLE OF INVENTION: PLANT GENE SEQUENCES I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT TILING DATE: 2002-11.15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR PILING DATE: 1999-09-13
PRIOR PLILATION NUMBER: 60/101,349
PRIOR FILING DATE: 1998-09-22
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR PLILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
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5. US20030101481A1
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Riechmann, Jose Luis
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Best Local Similarity 71.6%;
Matches 146; Conservative
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u, Guo-Liang
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Jiang, Cai-Zhong
Keddie, James
Zhang, James
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SEQ ID NO 145
LENGTH: 1009
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; OTHER INFORMATION: G801
US-10-295-403-145
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                                                                                                                                                                                                                                                                                                                                  -403-145
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LOCATION: (27)
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                                                                                                                                                                                                                                                                               269 GGATGCCTGCCACGTGTGCGGCTAGGATTTTCAATTAACTCGAGAGTTAGGTCACAAAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                               223 ccdarddrchadccaragadrddcircrccarcaadcrdadcrrrrarcaradccdcdd 282
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                                                                                                                                  0; Gaps
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APPLICANT: Rechmann, Jose Luis
APPLICANT: Heachmann, Jose Luis
APPLICANT: Hang, Cai-Zhong
APPLICANT: Adam, Luc J.
APPLICANT: Dubell, Arnold T.
APPLICANT: Dubell, Arnold T.
APPLICANT: Pineda, Omaira
APPLICANT: Puneda, Omaira
APPLICANT: Yu, Guo-Liang
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APPLICANT: Puneda, Omaira
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PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
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PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PUNBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: GB01
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eudicots; rosids
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Arabidopsis full.length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-I vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 486)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A.; Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shbata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                     Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Schences Center
3-1-1 Koyadai, Tenkuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4159
Fax: 81-298-36-4159
Email: meekiertc.riken.go.jp
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0; Mismatches 3;
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  Location/Qualifiers

1. 798

(organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO100DH3"
/dolone="ROHGA14"
/clone="ROHGA14"
/clone="lib="BOHG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

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Tel: 517-353-vec-
rex: 517-353-9168
Email: 2513.tcm@bm.cl.msu.edu
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Sed primer: T7 dye primer.
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MSU-DOB Plant Research Laboratory
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(Dases 1 to 373)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Benning, C
Dept. of Bacobnemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
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Michigan State University DNA Sequencing Facility Arabidopsis
Blobgical Resource Center, The Ohio State University, 309 Botany
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL 6142929371.
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                                                                                                                                                                                                                                              White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de larduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
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/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_l: EcoRl; Site_2: Xholl"
| 118 c 82 q 100 t
M28F8STM Arabidopsis developing seed Arabidopsis thaliana constitutione M28F8 5', mRNA sequence.
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Pred. No. 4e-103;
0; Mismatches 2; Indels
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lab_host="E.coli"
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clone="M28F8"
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strain="Columbia"
                                                                  BE522768.1 GI:9780746
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Best Local Similarity 99.5%;
Matches 362; Conservative
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Fax: 517 353 9334
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnaltae, Streptophyta; Embryophyta, Tracheophyta; Spermatophyta, Magnaltophyta, eudicoty, edons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

1. Gusea I to 335)

Newman, T., Gebrujin, F. J., Green, P., Keegstra, K., Kende, H., McIntosh, T.,, Ohirogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel Gene galoze: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                           12149 Lambda-PRL2 Arabidopsis thaliana cDNA clone 156J1T7, mRNA
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MSU-DOB-PRL, Michigan State University, Plant Biology Bldg., B
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Contact: Thomas Newman
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CACAGTGAGTCTCGAGGCCCAAGGCGGACGTNTNNATGCCGTCNTTTTCAATGTNTTTAGC 180 TCCACCGTCTTCGACAGGACCACCATGAAGAGCTTCGACTAAAGACCGTCACAGGA 242 TCCACCGTNTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACAGGA 240 GGTTGAAGGAAGAGAGAAGGATGCGGCTGCCACGAGGTTTTTCA 302		Db 477 Cy 528 Db 417 Ov 588	417 TGACGTGGCGGAAAATCCGGCGAAGAAGAGGACGTAAGGGACCTTCTACCAGTGAGTATAT 418 528 AGACATAAAGGACGCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAAC 510
			GATCCAACCTCCGCAAGCTCTGGCATCATCTGTGGGTCAAGAACTTCTGCCGCCAAGG
12-DEC-2 genomic	, , , , , , , , , , , , , , , , , , , ,	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	708 CTTGATTCCACAAATGGGGGTCGGTGGAATCAGCCTCAGTTATTAGCTTTTCCCGC 764 279 CTTGATTCAAAAGGTGGCCGTCGAACCAGCTCAGATATTAGCTTATCGGGCGC 220 765 CGCGGTGGTTCGCGTCGTCGTCGCGCGCTGTTCAACAGGCTTCCACGATGGCTAG 824 11
Mukaryota, Viralplantes, Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viralplantes, Streptophyta; Gudicota; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases I to 656) Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Umpublished Other GSSs: BOGDO41TF Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.	-	RESULT 6 235068 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE	Z35068 ATTS3707 Gif-SeedA Arabidopsis thaliana cDNA clone YAY344 5', mRNA aguence. Z35068.1 GI:510816 ZST. Arabidopsis thaliana (thale cress)
O E		ORGANISM ORGANISM AUTHORS TITLE JOHENAL COMMENT	Arabidopsis thaliana (Linear Cross) Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Sprmattophyta; Magnollophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Arabidopsis. CNRS. The Arabidopsis thaliana transcribed genome: the GDR cDNA program (Unpublished Contact: Berthomieu P., Guerrier D., Giraudat J. Genetique Moleculaire (Arabidopsis ISV - UPR40, CNRS Ayenue de la Terrasse, 1198 Gif-sur-Yvette Cedex, France Email: Giraudat@onre-gif.fr.
SogD" 1: pHOS1; Site_1: BstX1; 2-3 kb sheared inserted into pHOS1 using BstXI linkers" 190 g 157 t Score 311.2; DB 28; Length 656; Pred. No. 3.2e-87; Pred. No. 3.2e-87; Indels 46; Gaps 3;		FEATURES BOUTCE	Location/Qualifiers 1388 7788
	· · · · · · · · · · · · · · · · · · ·	BASE COUNT ORIGIN Query Match Best Local Matches 31 Qy 86 Db 1 Qy 146 Db 5	tch 27.3%; Score 292.6; DB 14; Length 388; 21.3%; Pred. No. 1.9e-81; 317; Conservative 0; Mismatches 5; Indels 2; Gaps 2 86 GAAACGTCGAAACTTCAAGACTTTCAAGATACCCAAGGTCTCGAGCCCAAGG 145

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103 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT
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Contact: Chris Town
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Best Local Similarity 73.9
Matches 309; Conservative
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Arabidopsis thaliana
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Bukaryota; Windiplanta; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (Bases II to 378)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
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Fax: 517 353 9334

Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Michigan State University DNA Sequencing Facility, 309 Bctany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
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Contact: Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                              BES23004
378 bp mRNA linear EST 19-MAR-2001
3186STM Arabidopsis developing seed Arabidopsis thallana cDNA
clone M31B6 5', mRNA sequence.
BES22004
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/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_l: EcoRl; Site_2: XhoII"
7 c 81 g 92 t
                                                                                                                                TACGGATGCCTGCCACGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACA
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Pred. No. 1.5e-69;
0; Mismatches 13; Indels 0;
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'dev stage="5-13 days after flowering"
'lab_host="E.coli"
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organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                  300 GCCACGGGTACGGGAACGGTTTCC 323
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strain="Columbia"
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Best Local Similarity 95.3%;
Matches 263; Conservative
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Brassica oleracea

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 725)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH543331 725 bp DNA linear GSS 14-DEC-2001
BOGCN02TF BOGC Brassica oleracea genomic clone BOGCN02, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       540 GGCCGITICAGCTICCICCGGTTTAGCTCCAATTGCCACGACGACGATCCAACCTCC 599
                                                          222
                                                                                                                                                                                                                                                                                                                           283 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGGGGCTTCGACTAAAGACGTCACACG 342
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                               GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
GATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
                                                                                                                                CCCACAGTGAGTCTCGAGGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA
                                                                                                                                                                                           223 cccacagraagrercaageeeaageegaageegageegargereererreaargeererrea
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/clone_Woctor: pHOS1; Site_1: BstXI; 2-3 kb sheared
/notes=Woctor: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkere"
1 198 c 191 g 154 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
SNG primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         241 AAGGTTGAAGGAAGAGGAGAAGGATACGGATGCCT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 AAGGGTTGAAGAAGAAGGATGAAGGATACGATGCCT 378
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/organism="Brassica oleracea"
/mol.type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOGCN02"
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145 ACCGGTOTTCOTTCOTCOTTCOTCOTCOTCOTCOTCOTCOTCOTC		571CATCCACCGGGCTCAACAACGCTGCCGCCAGGATGATT	Oy 655 CCGATGTGGGCTAFTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATT 714 Db 530 CCGATGTGGGCGTTTCCATCAAACGCAGTGGTTCCGACGGTTGAGACTTTCTTGTTGTT 471	Qy 715 CCACAAATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCT 771	Oy 772 GCTTCGCCGTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCT 831 410 GCTTTACCGTCGACGTCGCCGCCCTTCAGCAGGCTTCTTCTATGGCTAGACCACCCT 351	Oy 832 CCT 834 Db 350 CCT 348	17	ta; Embryophyta; Tracheog	edons; core trus. lerbacher,O.,Y.	រលស់សស	90978 : tin rime:		/dev stage="Mature Irule" /lab_host=="E. coll TJC11" /clone_lib="Washington Navel orange cold acclimated /flavedo & albedo cDNA library //acclimated	/ NOCESTY COLOR LANGUAGE AND EACH SET LANGUAGE SILE 1: ECORI; Sile 2: Xhoi; Plants were grown in the field at University of California, Riverside Agricultural Operations aince 1983: The scion was Washington Navel cannot and the rotetock Caristo from Carnot and the rotetock Caristo firsts I fissue from	mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately - 2 to 2 degree C. Approximately 2 cm median eartions of the rind were excised in the field from	several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort.	library was made, and 1 million primary fambda cDNA clones were in vivo excised to give a population of pbluescript
600 CCAACCTCCCCCTTCCCCCCCCCCCCCCCCCCCCCCC	-			-			÷										 . ·,
		ACCGGTCTCCGTTTCCTCCGGTTTAGCTC	GCAAGCICTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 65	GIGGGCIAITCCAICAAACGCAAIGAITCCGACGGICGGAGCIITCTICTIGAITCCACA 71	AATCGCTGGTCCGTCGAATCAGCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTC		SH470366 680 bp DNA linear GSS 13-DEC-2001 ON BOHCI33TF BOHC Brassica oleracea genomic clone BOHCI33, genomic N BH470366	DR4/0305.1 G1:1/6/84// GSS. Brassica oleracea SM Brassica oleracea Swaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids	; eurosids II; Brassicales; Brassicaceae; Brassica. E 1 (bases 1 to 680) S Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea L Unpublished Other GSSs: BOHCI33TR	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0192.org	DNA is from a doubled haploid provided by Seq primer: TF Class: sheared ends. Location/Qualifiers 1. 680	/organism="Brassica oleracea" /wol_type="genomic DNA" /strain="TOL000B3" /db_train="TOL000B3" /dlone="BOHG13" /clone="BOHG13"	/note="Vector: pHOS1; Site 1: BetXI; 2-3 kb sher genomic DNA inserted into pHOS1 using BstXI linl 145 a 188 c. 175 g 172 t	15.4%; Score 165; DB 28; Length 680; 72.5%; Pred. No. 9.5e-41; Ative 0; Mismatches 55; Indels 45; Gaps	ggtgaratetgatgargargargetarcetarcetetracrgtgagtatatagacata 	AGCGACGCTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGATCCAA	cctccccaagctctggcatcatccatgtggctcagcaacttctgccgcaaggaatgtat

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AW697442
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SK(-) phagemids. All steps to this point were performed in the TU Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an AB1350 at the Arizona Genomics Institute, University of Arizona (Collura Arizona Genomics Institute, University of Arizona (Collura Arizona Genomics Institute, University of Arizona (Collura Arizona Genomics Institute, University of Arizona (Collura Were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEsT pipeline (http://harvet.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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Arabidopsis thaliana
Bikaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Rispinolophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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An Arabidopsis full-length cDNA library was constructed essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AGAGCTTCGACTAAAGACCGTCACAAGGTTGAAGGAAGAGGAAAAGGATACGGATG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATCCGAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCACGGGT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAACCTTAAAAATCCCGACGACG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 ACTGGCACGGTCCCCGCTATCGCCGTTTCCGTTAACGGAACGTTAAAGATTCCCACAACG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 ACGAACGCTGATTCTGATATGGGTGAAAATCTGATGAAGAAGAAGGTAAACGACCTTCT
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                                                                                                                                                                                                                                                                                                                                                                         DB 14; Length 791;
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Pred. No. 1.6e-40;
0; Mismatches 91; Indels
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.ip
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Best Local Similarity 71.2%;
Matches 232; Conservative
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652 bp mRNA linear EST 15-JUN-2000
NF118G06ST1F1051 Developing stem Medicago truncatula cDNA clone
NF118G06ST 5', mRNA sequence.
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carrinci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 GTIAGGTCACAAATCCGACGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 GATAATTGAAGCAACCGGAACCGGAACTGTACCGGCTATTGCTGTATCGGTTAACGGAAC 426
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X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 AGGICGGAGGAICCGAAIGCCGGCGGGTIGCGCTGCTCGGGGTCTTICAATIGACCCGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.7%; Score 157.8; DB 9; Length 634; llarity 75.9%; Pred. No. 1.8e-38; Conservative 0; Mismatches 62; Indels 0
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula (barrel medic)
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Insert Length: 652 Std
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Fax: 580 221 7380
Email: radixon@nob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids; campanulids, Asterales; Asteraceae, Cichorioideae,
                                                                                                                                                                                                                                                                                                                                  195 GCAACCGGCACCGGCACGGTCCCTGCTATCGCGGTCTCCGTTGGTGGGACTCTCAAAATC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 CCGACGACGACGAACGCTGATTCTGATATGGGTGAAAATCTGATGAAGAAGAAACGTAAA 504
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                                                                                                                                                                                                                                                                                                                                                                                                375 ACAACCGGACGCGCATCCACCAAAGACCGCCACACAAAAGTGGAGGGCCGTGGCCGTAGG
                                                                                                                                                                                                                                                                         145 GCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTAGCTCCACCGTCTTCGACAGACCA
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                                                                                                                                              DB 14; Length 439;
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://ogpdb.ucdavis.edu/ for details.
Plate: QGCS row: H column: 15.
Location/Qualifiers
                                                                                                                                           Score 149.2; DB 14; Length
Pred. No. 7.9e-36;
0; Mismatches 153; Indels
                                               124
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/mol_type="mRNA"
/cultivar="Salinas"
          /note="Organ: apex"
98 c 126 g
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                                                                                                                                       Query Match
Best Local Similarity 62.0%;
Matches 254; Conservative
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Lactuca sativa
                                               91 a
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Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 439)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsai
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Contact: Tai C-J
Contact: Tai C-J
Dlant Biotech Research Center
Michigan Technological University, School of Forest Resources
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Fax: 906 487 2915
                                                                                                                      /organism="Medicago truncatula"
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/clone_lib="beveloping stem"
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/note="vector: Lambda Zap; Contains a mixture of internoal stem segments"
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/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
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Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                       Location/Qualifiers
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Location/Qualifiers
1. .439
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Best Local Similarity 72.9%;
Matches 199; Conservative
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/folone_lib="Gm-c1053"
/folone_lib="Gm-c1053"
/folone="Vector: pBluescript II SK+; Site_1: EccRI; Site_2: Xhol; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The CDNA library was constructed from mRNA isolated from whole seedlings of sweek old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dr) sequence with a xhol restriction site and a 3 anchor. EccRI adapters were ligated to the blunt-ended CDNA fragments followed by Xhol digestion. The CDNA fragments were directionally cloned into the EccRI-Xhol restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into DH10B host cells
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                                                                                                                                                                                                                                                                                                      /clone="GENOME SYSTEMS CLONE ID: Gm-c1053-1227"
tissue_type="Whole seedling, 3 week old, greenhouse
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp.

South Memorial Parkway Huntsville, AL 35801 For further ir

call: (800) -233-4363 or contact via email: ccu@resgen.com

Insert Length: 1706 Std Error: 0.00
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0; Mismatches 107; Indels
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'db xref="taxon:3847"
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                                                   /clone lib="0g ABCDI lettuce salinas"
/clone lib="0g ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. CDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size blas. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_ABCDI lettuce salinas
TAG_LISE=Llowers pre-fertilized
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stephce,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,Public Soybean EST Project
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Pred. No. 8.2e-35;
0; Mismatches 82; Indels
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Sequence 1034 from Patent WO0216655.
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AC051640 Homo sapi AL499604 Human BNA AC005241 Human BAC AF176350 Rattus no AF218846 Rattus no

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85961 103637

158514 160796 166983

AF383875 Mus muscu AF383875 Mus muscu AF286721 Rattus no AF286722 Rattus no AK695407 Sequence AC142506 Medicago Continuation (2 of Continuation (2 of AC010072 Homo sapi AC110593 Homo sapi AC110593 Homo sapi

Oryza sat Human DNA Mus muscu Medicago Trypanoso

AC016410 AC130432 AC007262 AC021414

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Virdiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
Stress-regulated genes of plants, transgenic plants containing REFERENCE AUTHORS TITLE is the number of results predicted by chance to have a

Pred. No.

PAT 27-SEP-2002

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DNA

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AL772401 Mouse DNA Homo sapi

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Patent: WO 0216655-A 1034 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
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LEPKAEPVMPSFSKASLAPPSSTGPPLKRASTKDRHTKVEGRGRRIRMPATCAARIFOL
TRELGHKSDGETIRWILENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTINADSDMGE
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PPLQVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTTHTLRDFSL
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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Submitted (17-APR-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
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protein.id="AAK43925.1"
db_xref="GI:13877695"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0; Indels 0;
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This clone was isolated by RT-PCR.
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/db_xref="taxon:3702"
/chromosome="II"
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                                                                                                                                                                                                                               GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGGTCACGG 240
                                                                                                                                                                                                                                                                                                                                                        TT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCTGATGAAGAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAAGCGAC 540
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                                                                                                                           CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTTCAATGTCTTTA 180
                                                                                                                                                                             121 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 180
                                                                                                                                                                                                                                                                                          GCTCCACCGTCTTCGACAGGACCACTTGAAGAGAGCTTCGACTAAAGACGGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                              241 AAGGTTGAAGGAAGAGGAGAAGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGAAACGATTCGGTGGTTGTTGGAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CAATTAACTOGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCCGCCATCGCCATG 420
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rosids, eurosids II, Brassicales, Brassicacea, ambryophyta, Tracheophyta, rosids, eurosids II, Brassicales, Brassicacea, Arabidopsis.

I (bases 1 to 1102)

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deno, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Carning, R., Yu, G., Bowser, I., Carning, R., Kan, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, I., Carning, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Mayaen, M., Palm, C.J., Sakurai, T., Baris, R. M., Schin, P., Southwick, A., Shinozaki, K., Baris, R. Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis chaliana
Arabidopsis chaliana
Bushidopsis chaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Nagnoliophyta; eudicotyledons; core eudicots;
rosids: eurosids'II; Brassicales; Brassicaceae; Arabidopsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The Riken Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA; RIKEN Arabidopsis Full-length cDNA'); Seki M.; Narusaka, M.; Ishida, J.; Satou, M.; Kamiya, A.; Sakurai, T.; Carninci, P.; Kawai, J.; Haysshizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MATIQKLEEVAGKDQTLRAVDLTIINGVRNVETSRPFQVNPTVS
Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M., Chang, C.H., Chang, E., Dale, J.M., Dang, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Mirenda, A., Dones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Mirenda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologie, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamada, K. (SSP/FORC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP /PGEC) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 [Dases 1 to 1102]

Yamada (K. Banh, J., Chan, M.M., Chang, C. H., Chang, E., Dale, J.M., Deng, J.M., Goldantth, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninoi, P., Chen, R., Cheuk, R., Hayashizaki, Y., Tshida, J., Ones, T., Xamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, Satou, M., Schinn, P., Southwick, A., Shinozaki, K., Bavis, R.W., Bcker, J.R. and Theologis, A., Shinozaki, K.,
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1. .1102
/organism="Arabidopsis thallana"
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ecotype: Columbia"
1. :1102
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db_xref="taxon:3702"

chromosome="2"
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. .1071
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                                                                                                 1.1 GI:21281084
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                                     mRNA, complete cds.
AY113981
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                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
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AUTHORS
                                                                                                                                                                                                                                                                                                                                            REFERENCE
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"E 2 (Dasses 1 to 1660)

S Yamada, K., Banh, J., Banno, F., Dale, J. M., Goldsmith, A. D., Lee, J. M., Omodera, C. S., Ouach, H.L., Tang, C. C., Toriumi, M., Yamamura, Y., Yu, S., Bowser, L. Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Kossema, E., Lin, J., Kan, C., Kossema, R., Lam, B., Lin, J., Sakurai, T., Marada, M., Narisaka, M., Nguyen, M., Pain, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S. E., Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A. Direct Submission

L. Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA, 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of Rafi, cDNA. RIKEN Arabidopsis Rill-Length DDNA.); Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Bayashizaki, Y. and Shinozaki, K., Carninci, P., Kawai, J., Rawai, J., Hayashizaki, Y. and Shinozaki, K., Carninci, P., Kawai, J., Kawai, J.,
                                                                                                                                                                                                                                                           961 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAAACAA 1020
                                                                                                                                                                                                                                                                                                  961 ATTGCAACAACGACGACGCACACGCTGAAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY056214 118-SEP-2002 MRNA linear PLN 18-SEP-2002 Arabidopsis thallana putative PCF2 DNA binding procein (At2g45680)
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            841 GTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTTAGCGGTTCGAATTTATCAAGA 900
                                                                                                                                              901 GCGACGTCGGTTATGGCTCCGAGGTCAAGCTCAGGGGTAACAACCGGTAGTTCATCGTCA 960
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDRAs: Yamada K., Banh,J., Banh,J., Dale,J., Dale,J., M., Goldanith,A.D., Lee,J.M., Onodera,C.S., Ouach,H.L., Tang,C.C., Toriumi, M., Yamamura,Y., Yu,G., Yu,S., Yu,S., Yu,S., Yosema,E., Lam,B., Lin,J., Meyers,M.C., Karlin-Neumann,G., Kim,C., Rosema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Bahm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total (Dases 1 to 1660)

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Lododsmith, A.D., Lee, J.M., Quach, H.L., Torlumi, M., Yu, G., Bowser, L. Carninci, P., Chen, H., Cheuk, K., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T. Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Bavis, R.W., Ecker, J.R. and Theologis, A., Shinozaki, K., Arabidopsis Full Length CDNA, Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta, Magnoliophyta, endicotyledons; core endicots, rosids; eurosids II; Brassicates; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCTTCACCAGTTCATGAGCACCACAAAGGCACGGTCATCGAACCACTGA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                           1021
                                                                                                   901
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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AY056214
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Matches 1071; Conservative
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Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence,
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Arabidopsis thaliana
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core;eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
1 (bases 1 to 91854)
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      643 GCCGTTTCAGCTTCCGGTTTAGCTCCAATTGCCACGACAACGATCCAACCTCCG 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
3. (bases 1 to 91854)
Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FSB-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598396.
Address all correspondence to:at@tigr.org
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The orientation of the sequence is from SP6 to 77 end of the BAC
                                                                                                                                            TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGTTCCACAA
                                                                                                                                                                                                 ATCCCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCCGCCGCCGCTGCTTCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCTTCACCAGTTCATGAGCACCACAACAACGACCATCGAACCACTGA 1173
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AC003680.3 GI:20197048
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LEPKAREVWDSFSMETAPPSSTGPPLARASTRORHTKTGRGRRINGPATCAPAIRO
LEPKAREVWDSFSMETAPPSSTGPPLARASTRORHTKTBRINGPATCAPAIRO
NLMKKRKRRPSNSEYIDIADAVSASSGAPIATTIQPPQALASSTVAQQLLORG
PMWALPSNAMIPTYAQQLLAGAGSGAPIATTIQPPQALASSTVAQQLGAGMA
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1174. . 1660
/gene="AL2g45660"
                                                                                                                                                                                                                                                                                                                                                                    trānslation="MATIQKLBEVAGKDQTLRAVDLTIINGVRNVETSRPPQVNPTVS"
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                                                                        /clone="RAFL07-08-P04 (R10678)"
/note="This clone is in a modified pBluescript vector (FLC-1) as a BamHI/XhoI insert.
ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
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/protein_id="AAL07063.1"
/db_xref="GI:15810351"
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/organism="Arabidopsis thaliana"
Nol_type="mRNA"
(db_xref="taxon:3702"
/chromosome="2"
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/evidence=experimental
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/gene="At2g45680"
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RIGIN
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4092. .4215,4582. .4712,4769. .4864,4948. .5188,5352. .5374,
5506. .5585,5670. .5980))
                                                                                                                                                                                                                                                                                                                                                                        /translation="MSFLRGIIDSFSSILNEESKKDPSVSSSSTSSESMGIDGUPVT
SERTAYKKKGYFDLAKEEIAKGYRAEBGHADDALLHYRNAGRIMMBATSTPSFSYIS
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SOKTPVARGGVATPPRYKDAASPRVKESGNYYDDKLVEMINTIUDRESPSYKWDDV
AGLNGAKQALLEMVILPAKRADLFTGLRRPARVTSLLGLLLFGPFGNGKTMLAKAVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESQATFRVVSASSLTSKWIDSIMSTRSTSENEASRRLKSEFLIQFDGVTSNPDDLVII
TAGANKRQEDEDAVLRRLYKRIYVPLDSNVRKLLFKTKLKCQPHSLSDGDIDKIVKE
TEGKLYKLCIKKHRFISGVTDKRYSGSDLQALCEEAAMMPIRELGANILTIQANKVLN
FSYSQINVEVCLSLKGLINRCVHVTGKISTI"
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INDVTFSHBEKTTDVNGFYDSTNBEALDEMHYLHAALSBTLRLYPDVPVDMRCAENDDV
LPDGHRVSKGDNIYTAMGRMTYIWGQDAEERPKDERMLKDGLFQPBSPFKFISFHA
GPRICLGKDPAYRQMKLVSMALLHFPRFRMADENSKVYYKRMITLHVDGGLHLCAIPR
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ATVFDLLFHSDELYDYETEIAREKPTYRFLSPGGSEILTADPRNVEHILKTRFDNYSK
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VSEFALSGKAFDAQDLLMRCTLDSI FKVGFGVELKCLDGFSKEGQEFMEAFDEGNVAT
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/gene="At2g45520"
/note="synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: F17K2.6; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="graynonym: F17K2.4"

join(<6429. .6950,7026. .7310,7386. .7724,7806. .8006,

8100. .8288)

/gene="At2g45510"

9100. .8288)

/gene="At2g45510"
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9289. .9356,9459. .>9632))
/gene="At2g45520"
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9289. 9356,9459. 9612))
/gene="At2g45520"
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/product=reputative cytochrome P450"
/protein_id="AAC06153.1"
/db_xref="G1:2979544"
                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAC06152.1"
/db_xref="G1:2979543"
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/protein_id="AACO6155.1"
/db_xref="GI:2979546"
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protein_id="AAC06154.1"
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complement (9578..9632)
/rpt family="(GA)n"
9822..1079
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/gene="At2g45510"
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1948. .10670
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gene="At2g45530"
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http://ccR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, of GlimmerM, See Minabela Pertea, of GlimmerM, see Minabela Pertea, http://genemark.biology.gatech.edu/GeneMark/), GlimmerM (a variant http://www.tigr.org/softlab/glimmerm.html/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mperteadrigr.org/, searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with BST similarity are named as unknown proteins. Genes without or BST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/Repeatmasker (Arian Smit, http.//ftp.genome.washington.edu/RN/Repeatmasker 
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NGGLFHGIHFSPDTVLGREGGFLGGWFTDNFRGREGGREGGRUDGKGNYLSGGYNLSGGYNL
HATHRGWKKHFYDTTHTDTALRGEDDDEFYLSLFSFGV"
COMPLEMENT (1002. . 2388)
GAGES-WASCATOTTHTDALRGEDDDEFYLSLFSFGV"
//Octe="Stages of the complement of the complement (1002. . 2388)
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HGGELYGVLKQNGHLTEQQAATYIASLSQALAYCHGKCVIHRDIKPENLLLDHGGRLK
IADFGWSVQSSNKRKTMCGTLDYLAPEMYENRDHDYAVDNWTLGILCYEFLYGNPPFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="DESKPSVQKFFPEVSDKCLEAAKFSSNRKNDIIARSREWKNMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MSKKSTESDAGNTEKQWSLADFEIGRPLGKGKFGRVYLAREAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1. .1281)
/note="overlap with BAC clone F4L23 (AC002387:1, .1281)."
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1655. .1750,1886. .2128,2260. .2388))
Genes Atzgats490"
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/mol_type="genomic DNA"
/cultivar="Columbia"
/db_xref="Loolumbia"
/chzomosome="2"
/map="CIC02E07"
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'protein id="AAF18607.2"
db_xref="G1:20197053"
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/note="synonym: F17K2.27"
join(<57. .242,335. .>747)
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/gene="At2g45500"
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oin(57. .242,33
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Location/Qualifiers
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AC006922.7 GI:20197941
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1. .2183
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SOURCE
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                                                                                                                                                                                /note="synonym: F17K2.7"
complement(join(<10833. 11272,11438. 11560,11636. 12378,
12454. 12937,13023. 13119,13254. 13374,13464. 13548,
13645. 13794,13957. 14073,14178. 14264,14350. 14576,14730. 14873,14178. 14264,14350. 14576,14730. 14873,14226. 14995,15396. 15538,
15768. 15244,16322. 16465,16545. 17093,17237, 170431,
17612. 17696,88015. 18613,18644. 19249,1963, 19714,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74472
          /trānslation="MOSSSSGGDDLEKOQOQOCKDKSPOKOSBSANESNHLTIVVCN
GDSSREELVGQIPPEKEVSLSRNGSSHEQCRVCLODKEEVLIELGCQCRGGLAKAHRS
CIDAWFRINSSNQCETCQVVANVYPPETQPTINYWWRIDDSYRQBERERGGFSPLW
VAFSILIGGLMLDVLISITLGVSALPVNIIIGVIVVLGLGTALRLTLEFCYEWSLRRA
VHRAVQRAZANNFSNIAYPPAL"
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                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Score 1071; Similarity 100.0%; Pred. No. 0; 1; Conservative 0; Mismatches
                                                                                                                            /rpt_family="(CAG)n"
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                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Simi
Matches 1071;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                         mRNA
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HTG
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparamicophyta; Magnoliophyta; eudloctyledons; core eudelocts;
Sparamicophyta; Magnoliophyta; eudloctyledons; core eucoide II; Prassicales; Brassicaces, Arabidopsis;
rosids; Lo 134151)
1 (bases I to 134151)
                                                                                                                  74411 ATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTCGCCG 74352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74171 ATTGCAACAACAACGACGCACGCTGAGAGACTTCTCCCCTAGAGATATACGAGAAAACAA 74112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r PLN 27-FBB-2002
g6825, complete
                                                                            TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCTTTACAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGCAACAACAACGCACACGCTGAGAGTTCTCCCCTAGAGATATACCAGAAACAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the bottom of the right arm of the chromosome between the ATHATPAS
                                                                                                                                                                                                                                                                                                                                                                                                 901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3. (bases 1 to 114151)
Town, C.D. and Kaul, S.
Direct Submission
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, ctownedigr.org
On Apr 18, 2002 this sequence version replaced gi:659638
On Oct B. 1997 this sequence version replaced gi:659638
On Oct B. 1997 this sequence version replaced gi:659638
On Oct B. 1997 this sequence version replaced gi:659638
On Oct B. 1997 this sequence version replaced gi:659638
Secondary of the sequence from the Rock of Secondary Submission contains the sequence from the Rock Secondary Dries
Submission contains the sequence from the Rock Secondary
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                                                                                                                                                                                                                                                                              74291 GTTGTTCCAAGCAGCGCTTTGTATCCGTTTCAAACGTTTGAATTTTATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   74231 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACCGGTAGTTCATCGTCA
                                                                                                                                                                                                                                        GTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (right end) to position 181918 of our previous Phase II submission YUPSH12 accession number AC000098. This fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGCITCACCAGTICATGAGCACCACAACAGCAGGTCATGAACCACTGA 74061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCTTCACCAGTTCATGAGCACCACACACACACGGTCATCGAACCACTGA 1071
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2 clone TlJ8 map g
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Arabidopsis thaliana chromosome
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mRNA

CDS

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.35311,35394. .35494,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(34048: .34414,35094, .35311,35394, .35494,
35596, .35809))
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       DTRELLGTVKRRNEVYEYLRDAIGDSMISYDIELVGPEITACSTSSSVAETLFSSDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORNILEEFIGKHGIRRPTILGVRHVFTGRVRNHYGHPDVFDRIFHITRGGISKAS
VINISBIJARGARRNSTERGANITHEDVGLIVALALESKYGAGGGGGTJRRDVKRI
OLEDFRANGSPETTVGRYCTARRSGADRAISRVAKLSGATALDAALARAGEVVGT
FTAVPMVMGFILELGLLKALFSFITMQFQLCSVFFTFSLGTRTHYFGRTILHGGARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGFRNLMGPOHORMDONALTIWLDRTSGSGFKSVKRPRSGYFGANITLOPGYYAGVIT
SLYLSNNEAHPGFHDEVDIEFLGTTFGKPYTLOTNVYIRGSODGKIIGREMKFRLWFD
PTKDFHHYAILWSPREIIPLVDDIPIRRYPKKSASTFPLRPMMLYGSIWDASSWATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKYKADYKYQPFTAKYTNFKALGCTAYSSARCYPLSASPYRSGGLTRQQHQAMRWYQT
HSWYNYCKDYKRDHSLTPRCWR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MGNSIISILSIFHLLVLWGSSVNAYWPPSPGYWPSSKYGSLNFY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: TiJ8.5, similar to cellulase (xyloglucan endo transglycosylase) (3.311355 from (Tropseclum majus) supported by full length cDNn: Ceres: 7831" complement (y full ,33824, .34414,35094.
                                                                                                                      YLLLYIAMTVEDFEDWYSWI.MYKGGYGYKGEISWESWREEGAHIOTLRGRILETI
LRFFWFQYGIVYKLDLIRKOYSLALYGYSWVVLVVIVFLFKGVASITFIALIVVAI
TDLSIPDWFACVLGFIPTGWALLSLAITWKQVLRVLGLWETVREFGRIYDAAMGMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="xyloglucan endotransglycosylase, putative"
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                                                                                                                                                                                                                                                                                                                              Complement (join 16114 1773,126628 16678,16797.
16997 17099,17634: 17773,17867 18025,18602 18879 18921,19083 19201,19620 19735,20017 2018 19301 120424,20823 20988,21079 21447,21292 21519 21628,21079 21687,21292 2018 21688,21711 21871,27202 27297))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPIALLSWFPF1STFQSRLLFNQAFSRGLEISI1LAGNRANVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'codon_start=1
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complement(33824':35833)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (31341, .31424) /gene="At2g36860"
                                                                                                       IPRSKIEEEVWKTLMGWE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |5596. .>35833)|
|gene="At2g36870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omplement (join (<10803. .11068,11697. .11765,12150; 12260,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym: T1J8.2; predicted by genefinder;supported by tull length cDNA: Ceres:108427: complement(join(<12752.13150,13249. 11533,13650. 13971,14054. 14159,14237. 14464,14576. .>14808))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               profein id="AAM15323.1"
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WWKHPNPVGGGFAMEAVLESAGPECVVPGQVTPLRLIGVKVWPVEVDLKFLEBVGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              omplement (join(13013. .13150,13249. .13533,13650. .13971,
4054. .14159,14237. .14464,14576. .14729))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
product="putative aquaporin (tonoplast intrinsic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement (join(11018. .11068,11697. .11765,12150. .12260, 2343. .12486))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ="MGILSDDVVIISQSEKEGDPSVITINCPDKTGLGCDLCRILLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLAIVRGDVSTDGKMCYLVFWVIGKPNTRWNLLKMRLVEASPSFSFSWAFGISRCYLSDS
ESQPPKLPDLFLIKLACSDRTGLLYDVTBVLYKLEINIEKVKISTTPDGKVMDLFFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="synonym: TlJ8.24; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                         note="synonym: TlJ8.1; supported by full length cDNA:
eres:36633"
oin(6605. .7052,7144. .7737)
note="overlap with BAC clone F13K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAGPLVGGGIAGLIYEVFFINTTHEQLPTTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="molecular marker ve017"
oin(6669. 7052,7144. 7515)
gene="At2g36830"
                                                                                                                                                                                                                                                                                                                                                                                                                      oin(6605. .7052,7144. .7737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="Expressed protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed protein"
d="AAD31570.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="At2g36835" .12597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKMLGKFMDNAVELMNKSFIDR"
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complement(10803. .1259
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774. .3801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540. 6996
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                                                                                                                                                                                                                                                                                                                                                  gene="At2g36830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="At2g36835"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement
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                                          repeat_region
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gene

mRNA

CDS

gene

mRNA

CDS

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38111. 38146
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complement(40567, .42581)

/rpt_family="AT_rich" 37801. .37845

repeat_region repeat_region

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BT008493.1 GI:30725659

JOCUS DEFINITION ACCESSION JERSION CEYWORDS

RESULT 7 3T008493

ORGANISM

RFERENCE AUTHORS

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DDRKQNENEXLKESETSGPTAA ÞMMAYA.PPSRSGAGNTFWML PVPTTAGNQMESSSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTSSTATATTTKRSTKDRHTKVDGRGRRIRMPALCAARVFQLTRELGHKSDGETIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sparmatophyta, Sparmatophyta, Sparmatophyta, Sparmatophyta, core eudicots, rooids, rooids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

(bases 1 to 1479)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Liam, B., Miranda, M., Palm, C.J., Southwick, L., Jones, T., Banh, J., Chen, H.; Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P. K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
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Direct Submission Source of the Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Second Seco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e-mail for correspondence: arab@sequence.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 8; Length 1206;
Pred. No. 6.2;
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                                                                                           pUNI
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                        /note="This clone is in
ecotype: Columbia"
1. .1206
                                                                                                                                                                                                                    /note="unknown protein"
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'chromosome="1"
'clone="U24662"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY081344.1 GI:19698994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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AY081344
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 1206)
S Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Ondera,C.S., Palm,C.J., Quach,H.L.,
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
Theologis,A. and Ecker,J.R.
Arabidopsis ORF clones
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Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
Naruiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Pallm.C.J., Quach,H.L.,
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamlya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nuyyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Pandad, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                             Query Match
2.3%; Score 25; DB 8; Length 134151;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana Atlg58100 gene, complete cds.
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(bases 1 to 1206)

TITLE JOURNAL EFERENCE AUTHORS

TITLE JOURNAL

COMMENT

/mol_type="mRNA"

EATURES

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Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081mit.edu/GBNSCAN.html), GeneMarkHam (Wark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant http://www.igr.org/sofilab/glimmerA httm/glimmerA.html, and GensEplicer (Wihaela Pertea.and Steven Salzbarg, contact mperteaghigr.org) searches of the complete sequence against a peptide database and the plant ESF database ar TIGR (http://www.tigr.org/tdh/tg! shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with shillarity to other proteins are named after the database hits. Genes without significant peptide similarity-but with EST similarity are named as unknown proteins. Genes without protein or EST similarity but with EST similarity are named as unknown proteins. Genes without protein prediction proteins genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl:edu/edy/RNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington-edu/RN/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYSVFEFATNAWKVTDHTRFHEKPELMDDSGRVSLNGNLYMTAYNSPHTGQYFIAMLD
FSKEIEKSRKTFCVLPCKGEKSTTHTRILGIYKGDRFSVLEGSKKTREIEIWVTKDQI
GNGDDGDDVVMIKEMTVSRPDFPILLSYISTSYFYDNDIHGKSFVLCCPSKRPKAAWV
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transcription factor, putative"
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EQGGGGVFAAHTSPLLGFHQLQHHQNQNQNQDPVETIPEGENFSRKRYRSVDLSKEN
DDRKQNENKSLKESETSGPTAAPMWAVAPPSRSGAGNTFWMLPVPTTAGNQMESSSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGRPEIMLNTHSHIYSISVDLKDENPTIKVRDLRFDHLSCRGYHLYGICDGNFPMXSF
LNGGGGVVWNPLFWRQTKWIAKAENTCGKAIGYDGSRPEKSYKIIGRSSCSWQGKVTD
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Poptonlglsmpdsnlgmlaalnsaysrggnananaeqannavehqekqqqsdhddds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to auxin induced basic helix loop helix transcription factor GI:5731257 from (Gossypium hirsutum)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="hypothetical protein, 5' partial"
protein id="AAG50757.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIVRGDLCKKIKIDQVLCEFQSSVYVPSLITIP"
complement (2159. .3364)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organiem="Arabidopsie thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="T18124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3567: .3595).
/rpt_family="AT_rich":
complement (4594. .4638).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="T18124.1"
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EQGGGGVFAAHTSPLLGFHHOLQHHQNQNQNDPVETIPBGBBFSRKRYRSVDLSKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTAAGHRAPPMWPFVNSAGGGAGGGGGAATHFWAGTGFSFPMDOYRGSPLOLGSFLAO
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Arblidopsis thaliana chromosome 1 BAC T18124 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (pases 1 to 85961)
Lin.X., Kaul,S., Town.C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnetead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome 1 BAC T18124 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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The orientation of the sequence is from SP6 to T7 end of the BAC
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Direct Submission
Submitsed (19-AUG-2000) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
3 (bases 1 to 85961)
Town, C.D. and Kaul, S.
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100.0%; Pred. No. 6.1;
ive 0; Mismatches 0; Indels
                                                                                                                                                               /clone="RAFL09-64-H20 (R24662)"
/note="This clone is in pBluescript
ecotype: Columbia"
                                                          organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                     note="synonym: T15M6.11"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                           1_type="mRNA"
_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TCGACTAAAGACCGTCACACGAA 239
     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                          gene="At1g58100"
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                                                                                                                                     chromosome="1"
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Best Local Similarity 100.0
Matches 23; Conservative
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                               source
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AC079131/c
LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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ORIGIN
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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TITLE
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JOURNAL
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FEATURES
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CDS

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YLDVAÑATNI SLTLONDFSYRNTVLSTORGVOELDRNKNAODAAFYSGASFIKKKSRO
RDSLVATGACPSWLPFARENGGGKNLGALYMSQDATVI SSERKNYAEPPSHDPKMLSS
EENNSNPSPVTYEADNTKRAKQQFAQRSRVRKLQYI SELERNVOTLQAEGSKVSAELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/protein_id="hypothetical"
/db_xref="GI:12321388"
/translation="MEIQRWRQLMSLWSNLKSSRVSLTGGNHTAASSADTFLKASRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FINORNI I LSMENKALKKRLESIAQĒKLIKOYSTVIKI VYLMSSVYYPVZOBVLEKRI
GRLRALYQQQQOTOKPSASRGRATSKDLDSQFSSLSINIKDSNCRRDSVSVMGPGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMGDKALFLSGGDDBVTVSSYSQTVIETDMLLVSASDQEMQSMVPDETFDFAFAÄSRH
DSABFIDRTLKVGGIFTVQLNLQDLPPNFLKHFNYEI VYVKSSEYTVMTMRKTGETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QXQSLVATGRKILGITEEDAREKALRKLEDVILEPPRAASRKSRTYFKRTRYLPDIMG
DNLDLBSYSRRVFIDVGNGKGSSGMEWFVENYPTRNQKFEMYXIETVNDEMSLESEKM
GMTEWLKENVKEEEYVVMKAZAEMVEEMMSKSIKMVDELFLECKPKGLGLGRGRKMQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLSLFWRSTLLALLFLSFTWLSLLKYGTTATAPSKSVESDLPELLPLLLNDLEKQGLF
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PENEGSLSQTQKDGLRDSRKRDKKALCLIYQGLDBDTFEKVVEATSAKBAWEKLRTSY
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                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="hypothetical protein"
/protein_id="AAG50761.1"
/db_xref="GI:12321383"
/translation="MASSKGSQSVRNLMYPGKHALLPPKIPPSSVSASYSBYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                      GSRHGQKLSNEKTHHQRTSSESHLVEELPFWLDDLLNEQPESPARKCGHRRSS
// Jene="118124.3"
// Jene="118124.3"
// Jene="118124.3"
// Jene="100ntains similarity to b2IP transcriptional
activator RSG GI:877512 from (Nicotiana tabacum)"
Complement (join(<5299. 5357,5415. 5651,5738. 5864,
5968. 6043,6135. >6853)}
                                                                                                                                                                                                                    complement(join(5299, .5357,5415, .5651,5738, .5864,
5968, .6043,6135, .6853)}
/gene="T18124.3"
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complement(12815. .13163)
gene="T18124.17"
/note="Pseudogene, putative heat shock transcription
factor HSP30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oduct="copia-type polyprotein, putative"

otein_id="AAG50765.1"

xref="GI:12321387"
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oin(<10149. .10243,10536. .>11703)
gene="T18124.4"
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gene="T18124,4"
codon ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (13870. .13965)
/rpt family="AT rich"
complement (14034. .14074)
/rpt family="AT rich"
complement (14182. .14205)
/rpt family="AT rich"
complement (14182. .14205)
/gene="Ti8124.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (8504. .8535)
/rpt family="AT rich"
complement (8599. .8627)
/rpt family="AT_rich"
10149. .11703
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I (bases I to 103637)

Lin,X., Kaul,S., Town,C.D., Benito,M.I., Creasy,T.H. Haas,B.J., Mul,S., Mail,R., Roming,C.M., Koo,H., Fujil,C.Y., Ufterback,T.R., Arabidopsis thallana chromosome I BAC TISMS genomic; sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMSYYLGIEVKQEDNGIFITOEGYAKEYLKKFKNDDSNPVOTPMEGGIKLSKKEEGEG
VDPTTFKSLVGSLRYLITCTRPDILYAVGYVSRYMEHPTTTHFKAAKEILRYIKGTVNF
GLHYSTTSDYKLVGYSDSDWGGDVDDRKSTSGFVFYIGDTAFTWMSKKQPIVTLSTCE
VLRSLDLKFEHIVTVIEETKDLEAMTIBQLLGSLQAYBEKKKKKBDIVEQVLNNQITK
BENGQSYQRRGGGQVRGRGRGGYGNGRGWRPHEDNTNQRGENSSRGRGKGHPKSRYDK
SSVKCYNCGKFGHYASECKAPSNKKFEEKANYVEEKIQEEDMLLMASYKKDEQEENHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEYVAATSCVCHAIWLRNILKELSLPQEBPTKIFVDNKSAIALAKNPVFHDRSKHIDT
RYHYIRECVSKKDVQLEYVKTHDQVADIFTKPLKREDPIKMSLLGVAKSSIRGGVES
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Arabidopsis thaliana chromosome I BAC T15M6 genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-SEP-2000) The Institute for Genomic Research, 9712. Medical Center Dr. Rockville. MD 20850. USA, cdrown@tigr.org 3 (bases 1 to 10367?)
Town.C.D. and Kaul.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC clone TISM6 is from Arabidopsis thallana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
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Similarity 100.0%; Pred. No. 4.4; Dength 85961;
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Arabidopsis thaliana
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own, C.D. and Kaul, S.
irect Submission
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/note="contains similarity to cell proliferation related protein GT:9931486 from (kins musculus)" complement(joint) 19207,19528 . 19647,19786 . 19886, 20080 . 20291,204618 . 19207,20502 . 20899;2128 . 21288 , 1891 . 22125,22528 . 22614)) complement(join(18837 . 19207,19528 . 19647,19786 . 19886, 20080 . 20291,20407 . 20787,20502 . 20989;21228 . 21288 , 21288 , 21288 . 21288 . 21288 . 22885, 22952 . 23614))
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/product="httpochetical_protein"
/product="httpochetical_protein"
/protein_id="AAG50696.1"
/db_xref="doi:123125."
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FRSELSSKNEWPDAPSPTAGSVDLADNIAAKSVAKVKKLKFSKAPEPRETLENDIDKS
SSQAVLEKPVVPVEKKEEPVPRLPERKPVFLNVYRKTKGIRIKSSKAVDGSSSVTEKS
ATDTVKKQDVVVGQXOTKTSERNSQASKKEABIATISLQKEEKKTDQNLRYNDELS
SLIVIKKINKGMEAADPRNVPWNPEALGIPDYFDIIKTPMDFGTICNNFEKGNKYMNSE
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RKEWRMKMORKFOVRNPOLLSLCETLFPNDNNHNSVWNGPHSLFRRGGSNRSSALHK
AVESLAMBLANSLSYALGARSLFAMLDESGYFHTLRAATSNASI FII STKAIGEYASL
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ASTKQKSHKRHGRHHKSDCMCAICVIKRRRRRRRBNSGAQEESSPAGSPSVDNSSVNM
GEDMDIDVDKKPEQEKITEIVELDSPVSKTQRVIENKQEVEEEENVEVESENKTKANVE
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AAVSIPVSPRITKPTEEGROSRSQSLLGVGMELWSPVAEIIRRSSEPSGCLVQSGDGA
ROQGWCGEIVLAMHCLCEVLLIRAPLCYL"
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'bseudo
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7463. .47681,47870. .48243,48329.
8927. .49132,49211. .49316,49403.
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/rpt family="(A)n"

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/rpt family="ATrich"

/rpt family="ATrich"

/rpt family="(Th)n"

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complement (24258. .24296)
/rpt_family="Ar rich"
complement (25863. .36393)
/gene="T15M6.5"
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complement(39499; 39523)
/rpt_family="AT_rich"
39684; 39709
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complement(40447, ...49696)
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complement(33893. .33928)
/rpt_family="AT_rich"
37880. .38594
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                                                                                                                                                                                                                                                           CDS
GeneSplicer (Wihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as unknown proteins. Genes without protein or EST similarity. That are predicted by more than two gene prediction programs over most of their longth are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wastingdon.edu/RM/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAIFAAIINRFKFTRWIILSIIGSILLIYVEGSPEFGGEPDENEEFYSTQAWITRAASI
AFALSICLEPQLCFEKYLVKTKRYGNKKVFRWIEMQICVSFVATVVCLVGLFASGENK
ELQGDSHRFKKGETYYVLSLIGLALSWQVWAVGLMGIVLYYGGVFGDVVHMCTSPLVA
LFVVLAFDFWIDDEFGRYTYOLLIGLATVVALGSYFYTLHKRNKKKWVELYQTENNIDV"
COMPLEMENT (6149. .6169)
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FLVLLGDSLVMLLLNFFYVQDNREDSDQDLQYRGTWLQALVQNAAFPLLIPLFFIFP
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/ rpt family="AT rich"
complement (1091. .2595)
/gens="T15%G.25"
/note="pseudogene, hypothetical protein"
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/gene="T15M6.26"
/note="pseudogene, hypothetical protein"
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/mol_type="genomic DNA"
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/db_xref="taxon:3702"
/chromosome="1"
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/rpt family="AT rich"
complement (10552. . 10573)
/rpt family="AT rich"
complement (10742. .10991)
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'protein id="AAG50699.1"
'db xref="GI:12321255"
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/gene="T15M6.24"
complement (<3359. ,>4729)
/gene="T15M6.24"
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complement (6713_ 6740)
/ Tpt_family="AT_rich"
complement (7047_ 7147)
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complement(12070..17708)
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/gene="T15M6.22"
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gene="T15M6.24"
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1864

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translation="MAPTKKPQKNKQSKNEIASSLIPNSGHKKPSKAPKLISPENED"
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Dermatophagoides farinae

Bukaryota; Metazoa, Arthropoda; Chelicerata; Arachnida; Acari;

Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;

1 (bases I to 2134)

1 (bases I to 2134)

Tsail.C., Chao, P.L., Shen, H.D., Tang, R.B., Chang, T.C., Chang, Z.N.,
Hung, M.W., Lee, B.L., and Chua, K.Y.

Isolation and characterization of a novel 98-kd Dermatophagoides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF352244 2134 bp mRNA linear INV 25-APR-2001
Dermatophagoides farinae paramyosin-like allergen mRNA, partial
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Direct Submission
Submitted (22-FBB-2001) Medical Research, Veterans General
HOSDital-Taipei, No. 201, Sec. 2, Shih-Pai Road, Taipei, Taiwan
112, Republic of China
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                         2.1%; Score 23; DB 8; Length 103637; 100.0%; Pred. No. 4.3; 0; Mismatches 0; Indels 0;
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8389668
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lin. Exp. Allergy 29 (12), 1606-1613 (1999)
0062524
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protein_id="AAG50700.1"
db_xref="G1:12321256"
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/db_xref="taxon:6954"
/clone="Derf11"
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Best Local Similarity
Matches 23; Consery
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AF352244
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AQQLEKK VAQUEKINLOLKYLLESYLEKQKSTLGYESTELQSEVEVLIMDLEKATRH
AQQLEKK VAQUEKINLOLKYLLESYLENGKSELEKVITELGACHESTEKLENDEN
QLARENKKYLDDLAARSKSGALADARRETHEOSIEIKRISMEDELSAAYKEBETLEKGE
EAKNORLIAELAQVRHDYEKRLAQXDEEIEALRKQYQIEIEQLNMRLAEAEAKLKTTE
ARLKKKYQAQTTELESLDAANKANTDLOKTIKKQALQITELQAHYDEVHKQLQQAV
QLGYTQRRCQALQAEIESHNIALBORNAKQAGLHEEAVVKYNELITINVALASAK
SKLESEESAACQADYBETHELBISDRANKAKGAEQLHEEAVVKYNELITINVALASAK
SKLESEESAALQAADBEHKELRISDRAVQKLTIELKSTKÖLLIEGORRUVKLETYVKKS
LEQEVRILHVRIEEVBANALAGGKRVIAKLESRIRDVEI EVEERRRAAGTOKLRKKK
BINRTVIELTSHKORLSQENTELIKEVHEVKLOLDNANHLKTQIAQOLEDTRHRLEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC124912 149452 bp DNA TINGAR HTG 16-JUL-2002 Papio anubis clone RP41-205M12, WORKING DRAFT SEQUENCE, 4 ordered
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O'Grooptinecinae, region.

Akhter, N., Antonellie, A., Ayele, K., Becketrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Laric, P., Haghighi, P., Hansen, N., Ho, S.-L., Idol, U.R., Karlins, B., Laric, P., Marguiles, B.H., Mastello, C., Makerni, B., Maduro, V. B., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M. B., Prasad, A., Schueleri, M. G., Stantripop, S., Thomas, J.W., Wetherby, K.D., Wiggins, L., Young, A., Schang, L.-H. and Green, B.D. NISC, Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC124912.2 GI:21844567
HTG; HTGS PHASE; HTGS DRAFT.
Paplo anubis (olive baboon)
Paplo anubis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cercopithecinae; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JUN-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 208777 USA 3 (bases 1 to 149452)
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Submitted (16-JUL-2002) NIH Intramural Sequencing Center, 8717

Grovemont Circle, Gaithersburg, MD 20877, USA

On Jul 16, 2002 this sequence version replaced g1:21465384.
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                                                                                                                                                                                                                                                                                                                                                                                 Score 22; DB 3; Length 2134; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

18748 18847: contig of 18747 bp in length 18748: 127485; contig of 108637 bp in length 127484; contig of 108637 bp in length 127484; contig of 108637 bp in length 127585 147017: contig of 19433 bp in length 147018 147018; contig of 19433 bp in length 147118 149421: contig of 2335 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone libe"RP41"
.44256
.note="Clone overlaps with GenBank Accession Number
.C125510 clone RP41-382N23 (center project name cyt.
        clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                  Insert size: 150000; agarose-fp
Insert size: 149152; sum-of-contigs
Quality coverage: 11.35x in Q20 bases; agarose-fp
Quality coverage: 11.42x in Q20 bases; sum-of-contigs
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Best Local Similarity 100.0%; Pred. No. 13,
Matches 22, Conservative 0, Mismatches 0, Indels 0,
                                                                                                                                                                                     Sequencing vector: plasmid, n/a, 100% of reads Chemistry: Dye-terminator Big Dye, 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 148556 bases at least Q40 Consensus quality: 148777 bases at least Q30 Consensus quality: 148773 bases at least Q20
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note="assembly_fragment"
27585. .147017
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note="assembly_fragment
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473 TGGGTGAAATCTGATGAAGAA 494

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Akhter, N., Antomellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dierrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N. Ho, S.-L., K., Karlins, B., Laric, P., Lee-Lin, S.-O., Legaspi, R., Maduro, G.L., Maduro, V.B., Maduro, V.B., Maduro, V.B., Maduro, V.B., Mastrian, S.D., Margulies, B.H., Masiello, C., Maskeri, B., Mastrian, S.D., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Teurgeon, C., Vogr, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D., Manner, J. M., C., Maskeri, C., Vogr, J.L., Walker, M.A., M., C., Maskeri, C., Vogr, J.L., Walker, M.A., M., M. C., Omparative Sequencing Initiative
Papio anubis clone RP41-382N23, WORKING DRAFT SEQUENCE, 4 ordered
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (28-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jul 20, 2002 this sequence version replaced gi:21622721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8% average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given however the sizes of the gaps between them are based on estimates that have
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Contact: nisc_zoo@nhgri.nih.gov
Contact: project Information
Center project name: cyt
Center clone name: 382N23
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1 (bases 1 to 170737)
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Homo sapiens chromosome 9 clone RP11-161B4 map 9, WORKING DRAFT
SEQUENCE; 25 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direction, S. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Baria, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodino, M., Doyle, M., Farreira, P., Fitzhidh, W., Gage, D., Galagan, J., Gardwin, S., Ginde, S., Grycette, M., Graham, L., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
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1 (bases 1 to 158514)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 9, clone RP11-16184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="clone overlaps with GenBank Accession Number AC124912 clone RP41-205M12 (center project name cyu)" 46239, .164110
//ote="assembly_fragment"
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Antes-clone overlaps with GenBank Accession Number
AC155511 clone RP41-427L1 (center project name cys)"
9020. 146138
as soon as it is available and
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          the accession number will be preserved.

1 89919: contig of 89919 bp in length

8920 90019: gap of unknown length

146139 146238: gap of unknown length

146239 146238: gap of unknown length

146239 16410: contig of 17872 bp in length

164211 164210: gap of unknown length

164211 170737: contig of 6527 bp in length

164211 170737: contig of 6527 bp in length.
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35046 c 32826 g 47413 t
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/clone="RP41-382N2"
/clone="RP41"
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132730. .170737
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/note="assembly_fragment
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Homo sapiens (human)
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AUTHORS
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AL Submitted (15-ARP-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Deases I to 15851).

Anderson, S. Linton, L., Nubbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boquslavkiy, L., Boukhalter, E., Brown, A., Burkett, G., Campoplano, A., Caselle, A., Choepel, Y., Colangelo, M., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhudi, M., Gage, D., Galgan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Illevi, J., Uohnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marquis, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Straus, C., Spencer, B., Stange-Thomann, N., Scrojanovi, M., Mison, D., Ye, W.J., Young, G., Zalnoun, J., Wilson, M., Targilio, J., Voung, G., Zalnoun, J., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZarthy, M., McZ
Levine, R. Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McBwan, P., McGurk, A., McRernan, K., McPheeters, R., Meldrim, J., Meneu, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., O'Noil, D., O'Livar, T.M., O'Livar, T.M., O'Lonnor, T., O'Donnell, P., O'Noil, D., O'Livar, T.M., O'Liver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Tteoders, S., Tteoders, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tteoders, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Polnay, G., Zainoun, J., Zimmer, A. and Zody, M., Kyman, D., Ye, W.J., Pinnert, Submission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatWasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 161 B 4

Center clone name: 16.1 B 4

Sequencing vector: M13; M77815; 93% of reads

Sequencing vector: Plasmid; n/a; %-0.f% of reads

6.5034429923489Chemiatry: Dye-terminator Big Dye; 100% of
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Consensus quality: 136255 bases at least Q40
Consensus quality: 147839 bases at least Q30
Consensus quality: 152536 bases at least Q20
Insert size: 159000; agarose-fp
Insert size: 156114; sum-of-contigs
Quality covverage: 3.4 in Q20 bases; agarose-fp
Quality cov.
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1783: contig of 1783 bp in length

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PRI 09-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL499604 160796 bp DNA linear PRI 09-MAR-2000
Human DNA sequence from clone RP11-23B15 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality datas of i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence assembly data is compared from overlapping clones.
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 2.0%; Score 21, DB 2, Length 158514,
1 Similarity 100.0%; Pred. No. 41;
21: Conservative 0; Mismatches 0; Indels 0:
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During sequence assembly
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Best Local Similarity
Matches 21; Conserve
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREKNEI, WORMPEP; Information on the WORMPEP database can be found at
                                                                                    http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                constructed by the group
                                                                                                                                                                                                                                                                                                This sequence is the entire insert of clone RP11-23B15 The true right end of clone RP11-54606 is at 35092 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIMC5 repeat: matches 7595. .7936 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7595 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 te="L1PB3 repeat: matches 5964. ,6141 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMC5 repeat: matches 6976. .7233 of consensus
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te="MER86 repeat: matches 25. .132 of consensus"
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.e="MLT1G repeat: matches 14. .536 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6. .8450
te="MER47A repeat: matches 2. .366 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2419 of consensus"
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.ote="MLT2FA repeat: matches 1. .400 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 14. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lote="SVA repeat: matches 552. .1259 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uSx repeat: matches 1. .310 of consensus"

    .4135
    .e="AluSx repeat: matches 2. .310 of consensus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER20 repeat: matches 1, .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   te="AluJo repeat: matches 1. .286 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .200 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 79. .130 of consensus"
                                                                                                                                                        Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9. RP11-23B15 is from the library RPCI-11.1 cor of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lone_lib="RPCI-11.1"
9. .503
                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:9606"
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ce="L2
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te="Al
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larlie4 repeat: matches 1795. .1952 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                       .1888 of consensus'
                                                                        note="L1M4 repeat: matches 3221. .3374 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 5433. .5742 of consensus
                                                                                                           note="AluSx repeat: matches 1....288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] repeat: matches 19. .137 of consensus"
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te="12 repeat: matches 1441. .1600 of consensus"
                                                                                                                                                                                                                                                                                                      e="AluSq repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="MLT11 repeat: matches 19. .134 of consensus"
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1126
                                                                                                                               5534: 16691
note="MIR repeat: matchem 18: 184 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 47. .240 of consensus"
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                                                                                                                                                                                        copies 2 mer aa 69% conserved"
                                                                                                                                                                                                                          note="25 copies 2 mer aa 98% conserved"
                                                                                                                                                                                                                                                                                                                                        copies 2 mer ag 72% conserved".
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                                      9. .954 of
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7. .22386
'evidence=not experimental
                                      repeat:
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ote="LIMB8 repeat: matches 5817. .6171 of consensus"
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ote="LIMB4 repeat: matches 5781. .6183 of consensus"
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708. .31108
note="L2 repeat: matches 2407. .2668 of consensus"
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Query Match 2.0%; Score 21; DB 9; Length 160796; Best Local Similarity 100.0%; Pred. No. 41; Matches 21; Conservative 0; Mismatches 0; Indels 0 CY 244 GTTGAAGGAAGAAGG 264

Search completed: February 2, 2004, 07:55:25 Job time : 4077.3 secs

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Arabidopsis thaliana; plant; gene; stress; transgenic; ds 👙
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Copyright (c) 1993 - 2004 Compugen Ltd
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stress condition to which a plant cell has been exposed plants with increased tolerance to these abiotic stresses Identifying a and producing

Claim 144; SEQ ID NO 1034; 577pp + Sequence Listing; English,

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and profile of expressed polynucleotides in the plant cell deharacteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to betwent by the European Patent Office.

Sequence 1071 BP; 287 A; 288 C; 256 G; 240 T; 0 other;

0; Gaps DB 24; Length 1071; 0; Indels 100.0%; Score 1071; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 1071; Conserv

09 9 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGGCGGTT ATGGCGACAATTCAGAAGCTTGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 61

GAICTAACCATCATCAACGGCGICAGAACGICGAAACTICAAGACCTITCCAAGIAAAT 120. GATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 61 121

CCCACAGTGAGTCTCGAGCCCCAAGGCGGAGCCGGTGATGCCGTTTTTCAATGTCTTTA 180 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAAGACCGTCACACG 121 181

AAGGTTGAAGGAAGAGGAAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTT 300 181 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGGGTTCGACTAAAGACCGTCACACC 241 AAGGTTGAAGGAAGGAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTT 241

301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG_360 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360 361 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGGCCATCGCCATG 420

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361 AACGCTGAGCCGCCGTTATAGCCGCCACGGTACGGGAACGGTTCCCGCCATCGCCATG 420

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ATTGCAACAACAACGCGCACACGCTGAGAGATTCTCCCTAGAGATATACGAGAAACAA 1020 GCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 960 721 ATCGCTGGTCCGTCGAATCAGCCTCAGTTATAGCTTTTCCCGCCGCCGCCGCTGCTTCCGCCG 780 781 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAA 840 TGGGCTATTCCATCAAAGGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAA 720 961 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1021 GAGCTTCACCAGTTCATGAGCACCACAAACAGCACGGTCATCGAACCACTGA 1071 781 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCT GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA 901 1021 901 961 品 名 品 8,5 8 6 8 8 ठ

ABX61156 standard; DNA; 460 26-FEB-2003 (first entry) ABX61156;

Thale cress; gene, ds; genetic manipulation; plant; biosynthesis; genetic modification; environmental stress; disease resistance; Arabidopsis thaliana polynucleotide #502

fungicide; insecticide; stress tolerance. Arabidopsis thaliana.

07-AUG-2001; 2001US-0924035 US2002142319-A1.

13-AUG-1999; 99US-148784P. 11-AUG-2000; 2000US-0638258.

HAMILTON C M. PRICE J.L. HARGISS T.R. MATHEW A V. LEDFORD B L. WOESSNER J P. RAMBAKA J G. (WOES/) (HAAS/) (GARC/)

Gorlach J., An Y., Hamilton CW., Price JL., Hargies TR., Yu Y., Rameaka JG., Page A., Mathew AV., Ledford BL., Woessner JP., Haas WD.; Garcia CA. GARCIA C

Novel Arabidopsis thalians nucleic acid useful for constructing

m

The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that modulate the capression or function of the polypeptides, for mapping functional capression or function of the polypeptides, for studying associated plants of the protein, in diagnosis, for studying associated plants are capable of witheraiding aparticular disease or chart cells, in screening assays of various plant strains that are capable of witheraiding a particular disease or environmental stress, for enhancing or inhibiting production of circumstants in products in plants and the sease resistance and stress are useful for introducing or improving disease resistance and stress collected in plants, screening biologically active agents, such as plant cells and plants. Screening biologically active agents, such as functional active agents, such as biosynthetic pathways of nutritional, commercial or medicinal value. Sequences ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS-ARSKOSSS transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes Claim 1; Page 158; 277pp; English. polynucleotides of the invention.

Sequence 460 BP; 113 A; 103 C; 134 G; 109 T; 1 other;

1019 629 839 899 GIGGGCTAITCCATCAAACGCAAIGAIICCGACGGICGGAGCIIITCIICIIGAIICCACA 719 AATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGGCCGCCGCNG-TTCGCC 282 222 959 GCAAGCTCTGGCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 401 AAICGCIGGICCGICGAAICAGCCICAGIIATIAGCITITICCCGCCGCCGCTGCTICGCC 779 AGTIGITCCAAGCAGCGCTITGTAICCGTTTCAGACGTTAGCGGTTCGAATTTATCAAG 162 AGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACCGGTAGTTCATCGTC 102 42 600 GCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT GTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACA AGTIGITCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAG Gredretracerececetrereacadecriceaceareceradaceacerecerraca AGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACGGGTAGTTCATCGTC 960 AATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACA Gaps 1, 27.0%; Score 289; DB 25; Length 460; 99.6%; Pred. No. 1.4e-131; 1; Indels 1020 AGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1060 41 AGAGCTTCACCAGTTCATGAGCACCACACAGCACGGTCAT 0; Mismatches Query Match Best Local Similarity 99.6 Matches 459; Conservative 340 006 460 999 00 720 780 281 840 221 161

ABL93850 standard; cDNA; 453 BP ABL93850; ESULT 3 BL93850/c

(first entry)

10-JUN-2002

Arabidopsis thaliana nucleic acid sequence Ref:2027615 SEQ ID NO:615.

Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;

genetic modification; gene; ss. 26-JAN-2001; 2001US-0770444. 27-JAN-2000; 2000US-178502P HAMILTON C M. PRICE J L. Arabidopsis thaliana LEDFORD B L. WOESSNER J P RAMBAKA J G. RAINES T M. MATHEW A V. GORLACH J. HURBAN P. US2002023280-A1. HOFFMAN PAGE A 21-FEB-2002 (ALLE/) (HOFF/) (HURB/) GORL/) ANYY/) YUYY/) (PAGE/) (WOES/) (HAAS/) (GARC/) KRIC/) SLAT/) DAVI/) LEDF/

Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y, Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD; Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N; Hurban P;

WPI; 2002-267486/31.

New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein

Claim 1; SEQ ID 615; 44pp; English.

The present invention describes an Arabidopsis thaliana nucleic acid (1) comprising a sequence capable of hybridising under stringent conditions to a sequence (51) sealected from any one of the 399 sequences given in ABL9328 to ABL94234. (1) have insecticide and fungicide activities, and identifying homologous or related genes; in producing compositions that identifying homologous or related genes; in producing compositions that modulate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physical pathways. (1) can also be used; (1), for the genetic manipulation of cells, particularly plant cells; (2) in screening assays of various plant strains to determine the strains that are best capable of withstanding a particularly plant cells; (2) in screening assays of withstanding a particularly plant cells; (2) in screening or inhibiting production of a losywitheric product in a plant; (4) as probes in mapping and in diagnosis in genetic modification and corrected to generate inboxymes or antisened coligonucleotides; and as single-stranded DNA probes or as triple-stand forming oligonucleotides; one specialization, but was obtained in electronic form at directly from the

5 - A - - -

Sequence 453 BP; 111 A; 100 C; 132 G; 107 T; 3 other;

Gaps .. 0 Score 286; DB 24; Length 453; Pred. No. 4.3e-130; 0; Indels Query Match
26.7%; Score 286; DB
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 286; Conservative 0; Mismatches

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ABQ47102/c ID ABQ47102 standard; DNA; 755.

ABQ47102;

(first entry) 12-JUL-2002 Oligonucleotide for detecting cytosine methylation SEQ ID NO 33693

ntral nervous system; cardiovascular; system; single nucleotide polymorphism; cytosine; diagnosis; Human; cytosine methylation; 5'-CpG-3'; uracil; side effect; cancer; central SNP; cell differentiation; ds drug; side effect; gastrointestinal;

Homo sapiens

WO200218632-A2

07-MAR-2002.

01-SEP-2001; 2001WO-EP10074.

01-SEP-2000; 2000DE-1043826 05-SEP-2000; 2000DE-1044543

(EPIG-) EPIGENOMICS AG.

K, Guetig D; Berlin Olek A, Piepenbrock C,

WPI; 2002-371829/40

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German:

This invention describes a novel method for determining the degree of methylation of a particular cytosine in, a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is tracted chemically to convert cytosine (C) but not methylated C', to uracil, then part of the genomic DNA that contains the target C is amplified to form, a labeled amplicon. Far application to be petided nucleic action from member, of oligonucleotides and/or peptide-nucleic act (PNA) cilgomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the levino classes of oligomers, the degree of methylation is calculated The method is used: (1) for diagness and/or prognosis of side effects of the method is used: (1) for diagnesis and/or prognosis of side effects of disorders therapeutic

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5-CpG-3', present in a genomic ample of DNA. The sample is tracted chemically to convert cytosine ample of DNA that occurrent the methylated C' to uracil them part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or upptied-nucleic acid (PNA) oligoners and the degree of hybridises and/or upptied-nucleic acid (PNA) oligoners and the degree of hybridised to the two classes of oligoners, from the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the method therapeutic drugs and of a wide range of diseases; e.g. cancer, disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f a wide range or unserged cardiovascular, gastrointestinal and respiratory or addiovascular, by by detecting mutations or single nucleotide
                 types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined similtaneously a8Q13410-ABQ54121 represent genomic DNA sequences used to illustrate themethod for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug, side effect, cancer, central nervous system, cardiovascilar, gastrointestinal, respiratory system, single nucleotide polymorphism, SNP, cell differentiation, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for detecting cytosine methylation SEQ ID No 33694
polymorphisms (SNP's); and (ii) for differentiation of cell or
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                                                                                                                                                                      2.0%; Score 21; DB 24; Length 755; 100.0%; Pred. No. 5; ative 0; Mismatches 0; Indels C
                                                                                                                                         Sequence 755 BP; 125 A; 78 C; 282 G; 270 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytosine methylation; 5'-CpG-3';
                                                                                                                                                                                                                                                              438 AAAAATCCCGACGACGACGAA 458
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                                                                                                                                                                                                                                                                                              88 AAAATCCCGACGACGAA 68
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05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                Best Local Similarity 100.0% Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         duman; cytokine; cell proliferation; cell differentiation; growth factor;
ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                                      2.0%; Score 21; DB 24; Length 755; .00.0%; Pred. No. 5;
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                                                                                                                                                                                                                                 Sequence 755 BP; 270 A; 282 C; 78 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 5; Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AAAAATCCCGACGACGACGAA 458
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.D ABA08516 standard; cDNA; 453 BP.
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27-APR-2000; 2000US-0560875.
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P-PSDB; ABB11272.
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contraction or chemokinetic activities, haemostatic, thrombotic or chemokinetic activities, haemostatic, thrombotic or thrombolytic activities, polypeptides and nucleotides of involved in oncogenesis, cancer cell proliferation or metastasis.

Conditions, e.g., by brotein or gene therapy: Such conditions include conditions, e.g., by protein or gene therapy: Such conditions include ancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders, inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease.

Conditions, e.g., by properides (e.g., osteoporosis), and abnormal arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, inclains and ulcers), while those with bacterial and fungal infections in addition to immune disorders.

Confort or or cell growth, For example, such polypeptides may be used to convert the can be used to augment or resplace cells damaged by illness, cantorimmune disease or accidental damage. The polypeptides and in the disapness of the above conditions, and indrug screening techniques. The present expresents a cDNA encoding a convert way also be used in the disapness of the above conditions, and in drug screening techniques. The present expresents a cDNA encoding a novel human polypeptide of the invention.
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have various activities, including cytokine, cell proliferation or differentiation activities, stem cell growth factor activity, haematopolesia regulators activity, tissue growth activity, immunomodulatory activity, activity, or inhibin-related activities;
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Pred. No. 16;
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100.0%; Pred. No. 1...
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
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99US-0128234.
99US-0128714.
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99US-0130077.
99US-0130449.
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Best Local Similarity 100.C
Matches 20; Conservative
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PR 20-7UL-1999; 99US-0144632

PR 21-7UL-1999; 99US-0144884; PR 21-7UL-1999; 99US-0144684; PR 22-7UL-1999; 99US-0144684; PR 22-7UL-1999; 99US-0145086; PR 22-7UL-1999; 99US-0145086; PR 22-7UL-1999; 99US-0145086; PR 22-7UL-1999; 99US-0145082; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 22-7UL-1999; 99US-0145218; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0144328; PR 02-7UL-1999; 99US-0154338; PR 02-7UL-1999; 99US-0154338; PR 02-7UL-1999; 99US-0154338; PR 02-7UL-1999; 99US-0154338; PR 02-7UL-1999; 99US-0154339; PR 02-7UL-1999; 99US-0154339; PR 02-7UL-1999; 99US-0156358; PR 02-7UL-1999; 99US-0156358; PR 02-7UL-1999; 99US-0156358; PR 02-7UL-1999; 99US-0156358; PR 02-7UL-1999; 99US-0156358; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-7UL-1999; 99US-0156359; PR 02-
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99US-0132486.
99US-0132487.
99US-0134256.
99US-0134218.
99US-0134218.
99US-0134219.
99US-0134370.
99US-0134941.
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99US-0135124.
99US-0135629.
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100.0%; Pred. No. 50;
ive 0; Mismatches 0; Indels
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99US-0159637.
99US-01595838.
99US-0160781.
99US-0160767.
99US-01607767.
99US-01607767.
99US-0160914.
99US-0160918.
99US-0160918.
99US-0161404.
99US-0161406.
99US-0161406.
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99US-0123180.
99US-012348.
99US-0126264.
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99US-0126263.
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99US-0129845.
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99US-0130449.
99US-0130510.
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990S-0132448.
990S-0132407.
990S-0132484.
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                                                                                                                                                                                                                                                                                             Local Similarity 100.
les 19, Conservative
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21-0CT-1999
21-0CT-1999
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22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
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09-MAR-1999;
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01-APR-1999;
06-APR-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
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Best Local S
Matches 19
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22-UUL-1999 99US-0145089 99US-01419192 99US-0141145 99US-0141192 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-0141145 99US-
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The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect, cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 30293
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0
                                                                                                                                                                                                                                  DB 21; Length 499; 49;
                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 49;
ive 0; Mismatches
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ABQ43702/c
ID ABQ43702 standard; DNA; 600 BP.
99US-0160814.
99US-0160815.
99US-0160981.
99US-0160981.
99US-0161404.
99US-0161406.
99US-0161369.
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05-SEP-2000; 2000DE-1044543.
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Best Local Similarity 100.0%
Matches 19; Conservative
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28-OCT-1999;
29-OCT-1999;
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is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                                                                                                                      Sequence 600 BP; 136 A; 53 C; 216 G; 195 T; 0 other;
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100.0%; Pre
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Best Local Similarity 100...
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24; Length 600; 0; Indels This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptidenucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the repout the range of diseases, e.g. cancer, disorders

f diseases, e.g. cancer, disorder gastrointestinal and respiratory

the central nervous, cardiovascular,

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systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13411. Tepresent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                              Score 19; DB 24; Length 600;
Pred. No. 49;
                                                                                                                                                                             0; Indels
                                                                                                                 Sequence 600 BP; 195 A; 216 C; 53 G; 136 T; 0 other;
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1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                       441 AATCCCGACGACGACGAAC 459
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990S-0139763.
990S-0139817.
990S-0140353.
990S-0140353.
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990S-0141287.
990S-0141287.
990S-0141842.
990S-0142154.
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99US-0139463.
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99US-0139459
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99US-0137222
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99US-0139454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for sematic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and proteczoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. multiple sclerosis), meningitis, abscesses, prion diseases (e.g. multiple sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, myopathy, myasthenia gravis, and mental disorders (e.g. Tourette's syndrome). CDNA sequences ABL99929 represent human secretory polymucleotides of the invention.
                                                                                                                                                       Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; Peralta CH, David MH, Panzer SR, Flores V, Daffo A; Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 908 BP; 225 A; 214 C; 184 G; 285 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 349; 585pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             988 AGAGACTICICCCIAGAGA 1006
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07-SEP-2000, 2000US-230951P.
07-SEP-2000, 2000US-231163P.
07-SEP-2000, 2000US-231832P.
                                                                                                       (INCY-) INCYTE GENOMICS INC.
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P-PSDB; ABB97909.
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05-MAR-1999;
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15. UL. 1999; 99US-0144008.

18. 15. UL. 1999; 99US-0144008.

18. 19. UL. 1999; 99US-0144325.

18. 19. UL. 1999; 99US-0144332.

18. 19. UL. 1999; 99US-0144332.

18. 19. UL. 1999; 99US-0144332.

18. 20. UL. 1999; 99US-0144333.

18. 21. UL. 1999; 99US-0144333.

18. 21. UL. 1999; 99US-0144334.

18. 21. UL. 1999; 99US-0144334.

18. 21. UL. 1999; 99US-0144334.

18. 22. UL. 1999; 99US-0144632.

18. 22. UL. 1999; 99US-0144334.

18. 22. UL. 1999; 99US-0144334.

18. 22. UL. 1999; 99US-0144334.

18. 22. UL. 1999; 99US-014508.

18. 22. UL. 1999; 99US-014508.

18. 22. UL. 1999; 99US-014508.

18. 22. UL. 1999; 99US-014508.

18. 22. UL. 1999; 99US-014508.

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18. 22. UL. 1999; 99US-014508.

19. UL. 1999; 99US-014508.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

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19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

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19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1999; 99US-014919.

19. UL. 1990; 99US-014919.

19. UL. 1990; 99US-014919.

19. UL. 199
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Gaps
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Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      224 CTAAAGACCGTCACACGAA 242
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9908 - 0158232

9908 - 0158232

9908 - 0159293

9908 - 0159329

9908 - 0159329

9908 - 0159329

9908 - 0159331

9908 - 0159638

9908 - 0159638

9908 - 0159638

9908 - 0160741

9908 - 0160767

9908 - 016078

9908 - 016081

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99US-0161360.
99US-0161361.
99US-0161992.
99US-0161992.
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9908-0123180.
9908-012548.
9908-0125788.
9908-0126264.
9908-0126785.
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AAC43180
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9US-012984	9US-013007	9US-013044	9US-013051	9US-013089	908-013144	911S-013240	9US-013248	9US-013248	9US-013248	9US-013248	9US-013286	9US-0134256	908-0134218 610-0134218	908-0134219	908-0134221	9US-01345768	9115-0134768	9115-0135124	911S-0135353	9US-0135629	9US-0136021	9US-0136392	9US-0136782	9US-0137222	9US-0137528	9US-0137502	9US-0137724	9US-0138094	9US-0138540	9US-0138847	9US-0139119	9US-0139452	9US-0139453	9US-0139492	9US-0139454	9US-0139455	903-0139436	9US-0139458	9US-0139459	9US-0139460	9US-0139461	9US-0139462	9US-0139463	9US-0139750	9US-0139763	9US-0139817	9US-0140353	9US-0140354	9US-0140695	9US-0140823.	9US-0140991	908-0141287	9US-U141642 9IIS-0142154	9US-0142055	9US-0142390	9US-0142803	9US-0142920	9US-0142977	9US-0143542	9US-U145624 9TS-0144005	9US-0144085	9US-0144086	9US-0144325	9US-0144331	9US-0144332	9US-0144333	
6-APR-1999;	9-APR-1999;	1-APR-1999;	3-APR-1999;	3-APR-1999;	0-AFK-1999; 0-AFR-1999;	0-APR-1999;	4-MAY-1999;	5-MAY-1999;	6-MAY-1999;	6-MAY-1999;	7-MAY-1999;	1-MAY-1999;	4-MAI-1999;	A - MAY 1000.	4 - MAY - 1999; 4 - MAY - 1999;	8-MAY-1999;	9-MAY-1999;	0-MAY-1999;	1-MAY-1999;	4~MAY-1999;	5-MAY-1999;	7-MAY-1999;	8-MAY-1999;	1-JUN-1999;	3-JUN-1999;	4-JUN-1999;	7-JUN-1999;	8-JUN-1999;	16661-NOO-0	1555 - NOO-0	4-JUN-1999;	6-UUN-1999;	SOUT-NOO-9	1 5 5 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	S-CUN-INCO.	0-00N-1999;	. 6661 - NIL: - 8	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	8-JUN-1999;	1-00N-1999;	3-JUN-1999;	3-JUN-1999;	4-JUN-1999;	28-JUN-1999, 9	9-JUN-1999;	. 4444 - 1111 - L	1~100-1333; 1~1TT-1999;	2-JUL-1999;	6-JUL-1999;	8-JUL-1999;	9-JUL-1999;	2-JUL-1999;	3-00L-1999;	7 - 100m - TH 1000 - 5	6-JUL-1999;	6-JUL-1999;	9-JUL-1999;	9-JUL-1999;	9-JUL-1999;	9-JUL-1999;	
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Human; ss; gene; secretory protein; secretory polynucleotides; SPTM; SPTM-related disease; somatic gene therapy; germinine gene therapy; servial act disease; somatic gene therapy; germinine gene therapy; servial combined immunodeficiency; intracellular parasite protection; fungal parasite; protozoan parasite; cell proliferative disorder; ancer, montor neuron disorder; neurological disorder; parkinson's disease; meningitis; abscess; prion disease; cerebral palsy; neuroskeletal disorder; peripheral nervous system disorder; dermatomyositis; polymyositis; myopathy; myasthenia gravis; mental disorder; Potrette's syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 21; Length 1893;
Pred. No. 45;
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100.0%; Pre
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ABL99921 standard; cDNA; 2794 BP
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2000US-230583P.
2000US-230505P.
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Best Local Similarity 100.
Matches 19; Conservative
99US-01
99US-01
99US-01
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99US-01
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05-SEP-2000; 2
06-SEP-2000; 2
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05-SEP-2000; 2
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05-SEP-2000; 2
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BL99921/c
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The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA acquences are useful for somatic or combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. fungal steases), motor neuron disorders, demyelinating diseases (e.g. multiple scleosis), meningitis, abscesses, prion diseases (e.g. multiple scleosis), meningitis, and polymyositis, myasithenia gravis, and mental disorders (e.g. Tourette's syndrome), cDNA sequences ABL99746 - ABL99929
                                                                                                                                                                                                                                                                                                                                                                    Hillman JL;
Dahl CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polymucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites -
                                                                                                                                                                                                                                                                                                                                                                 Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR, Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; Gersein EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A; Marwaha R, Chen AJ, Chang SC, Au AP, Inman'RR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent human secretory polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2794 BP; 704 A; 656 C; 549 G; 885 I; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. Mc. 100.0%; Prec. Mc. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 360-361; 585pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             988 AGAGACTICTCCCTAGAGA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL14198 standard; cDNA; 15987 BP
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                                                               000US-230595P.
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                                                                                                  000US-230597P
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07-SEP-2000; 2000US-231832P
                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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Best Local Similarity 100.
Matches 19, Conservative
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P-PSDB; ABB97925.
                                                                                                                                               06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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ABL14198
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26-MAR-2002 (first entry)

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
Drosophila melanogaster expressed polynucleotide SEQ ID NO 37076.
                                                                   Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15987 BP; 4295 A; 3570 C; 3827 G; 4295 T; 0 other;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                        Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75.
P-PSDB; ABB70095.
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Search completed: February 2, 2004, 03:13:24 Job time : 317.239 secs

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0; Gaps

0; Indels

DB 23; Length 15987; 40;

Query Match
1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches

us-09-938-842a-1034.oli.rst

10.1 335 14 3.5 586 28 3.5 798 28 3.3 656 28	3.0 600 28 2.2 318 9	2.22 2.22 2.22 2.22 2.22 2.22 2.22 2.2	23 2.1 222 10 BB052744 23 2.1 222 10 BB052744 23 2.1 222 10 BB052810 23 2.1 224 10 BB057092 23 2.1 224 10 BB057092	2.1 232 10 2.1 233 10 301 10	2.1 381 13 2.1 380 13	2.1 395 13 2.1 415 14	2.1 435 13	2.1 479 13	2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0 2.0	2.0 567 9	2.0 747 13 1.9 146 28	1.9 208 28 1.9 278 29	1.9 339 28	1.9 377 10	1.9 400 14		ALIGNMENTS		20000000000000000000000000000000000000	M28F8STM Arabidopsis develop	BE522768	DESTANCE OF CENTRAL MANAGEMENT OF CENTRAL MA	Arabidopsis thallana	Eukaryota, Viridiplantae, Streptophy Spermatophyta, Magnoliophyta, eudico	; eurosids II; Brassicales; Brassica 1 (bases 1 to 373)	White, J. A., Todd, J., Newman, T., Fody Ilarduya, O., Jaworski, J.G., Ohlrogge A new set of Arabidopsis expressed	seeds. The metabolic pathway from caplant Physiol. 124 (4), 1582-1594 (2	20567808 11115876 Contact: Benning, C	Dept. of Biochemistry & Molecular Bi Michigan State University	224 Blochemistry, Michigan State Uni , USA Tel: 517 355 1609
n n n i π n ν ν ν		0 1 4 4 4 1 5 6 4 1	4 H H H F	0 1 C	1 0 0	25 26	227	 6 0 F		ກ ດ ດ ດ ດ ດ ດ ດ ດ ດ		8 6 8 7 0	0 4 4 0 14 4 4 14 14 14 14 14 14 14 14 14 14 14) O O			E HIODO	BE522768	DEFINITION	ACCESSION	KEYWORDS	ORGANIS		REFERENCE	AUTHORS	JOURNAL	MEDLINE PUBMED COMMENT		
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5.1.6 Compugen Ltd.		earch time 2477.95 Seconds hout alignments) 4.671 Million cell updates/sec	.cacggtcatcgaaccactga 1071		es		3: 45562784																			cted by chance to have a of the result being printed, score distribution.		Description	BE522768 M28F8STM	AV825375 AV825375 BEE23004 M31B6STM Z35068 ATTS3707 Gi
GenCore version 5.1. Copyright (c) 1993 - 2004 Comp	ic search, using sw model	February 2, 2004, 00:53:06; Search (without a 10504.671	US-09-938-842A-1034 1071 1 atggcgacaattcagaagct	OLIGO_NUC Gapop_60.0 , Gapext 60.0	22781392 seqs, 12152238056 residues		ts satisfying chosen parameters	length: 0 length: 2000000000	isting first 45 summaries	BST:*	em_esthum:* em_estin:*	em_estmu:* em_estov:*	em_estpl:* em_estpl:*	em_btc:*	95 cst:: 95 est2:* 95 btc:*	gb est3:*								7: em_gss_vrl:* 3: gb_gssl:*		. No. is the number of results predicted e greater than or equal to the score of t is derived by analysis of the total score	SUMMARIES	% Query Match Length DB ID	373 10	29.9 486 9 AV85335 22.8 378 10 BB523004 20.9 388 14 Z35068
o.	√ nucleic - nucleic	ın on: Fe	itle: US erfect score: 10 equence: 1	oring table: OL Ga	sarched: 22	ord size : 0	stal number of hit	inimum DB seq len eximum DB seq len	ost-processing: Li	atabase : E		5.5	9:	. co o	71		. T	9 7	, H	i 8 5	7 77 6	1 2 2	, v,	,	52	Pred. No. is score greate and is deriv		esult Score Mo. Score Me	334	2 320 2 4 224 2

EST 19-MAR-2001 liana cDNA	Tracheophyta; udicots; rosids s. Martinez de C. C. m developing	msing, MI 48824
mRNA linear	phyta, Embryophyta, icotyledons, core e icaceae, Arabidopsi ocks,N., Girke,T., ge,J. and Benning, ge,J. and Benning, ae,J. and Benning, carbohydrates fro carbohydrates	ular Biology ate University, Bast La
BES22768 M28FSTM Arabidopeis developing seed Arabidopsis thaliana cDNA clone WBRFS 5, mRNA sequence. BES22768 GISS22768.1 GI:9780746	Arabidopsis thaliana (thale cress) Arabidopsis thaliana Eukaryota; Viridiplainae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplainae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; i eurosida II; Brassicales; Brassicaceae; Arabidopsis. i (bases II; Brassicales; Brassicaceae; Arabidopsis. White, J. A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de White, J. A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de A new set of Arabidopsis expressed sequence tags from developing seede. The metabolic pathway from carbohydratesto seed oil physical physiol. 124 (4), 1582-1594 (2000)	C stry & Moleci iversity Michigan St.
BES22768 M28F8STM Az Clone M28F8 BES22768 BES22768.1	Arabidopsis thaliana Arabidopsis thaliana Bukaryota; Viridiplai Spermatophyta; Magnoi (base 11; Brass; White, J. A., Todd, J., Ilarduya, O., Jaworsk; A new set of Arabido A new set of Arabido Beeds. The metabolic Plant physiol: 124	11115876 Contact: Benning, Dept. of Blochemin Michigan State Uni 224 Blochemistry, USA Tel: 517 355 1609
RESULT 1 BE522768 LOCUS DEFINITION ACCESSION VERSION KEYMORDS	SOURCE ORGANISM ORGANISM AUTHORS TITLE JOURNAL	PUBMED

9071108

FEATURES

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MJIB6STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M31B6 5', mENA sequence.
BE523004.1 GI:9780982
1-11 Koyadai, Taukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-906
Fax: 81-298-36-906
Fax: 81-298-36-906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCCACAGTGAGTCTCGAGGCCCAAGGCGGAGCCGGTGATGCCGTTCTTAATGTCTTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 GATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACGGTCACACG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 AAGGITGAAGGAAGAGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTT 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
edons; core eudicots; rosic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RAFL7"
/note="Site_1: BamH1; Site_2: Sal1; subjected
cold-treated (1, 2, 5, 10, 24 hr)"
118 c 117 g 117 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Ti
Spermatophyta, Magnoliophyta, eudicotyledons, core eudi
9 eurosida II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 378)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Marabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.486
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/db xref="taxon:3702"
/clos="RAFL07-08-P04"
/dev stage="rosette plants"
/lab_host="DH108"
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100.0%; Pred. No. 4.5e-166;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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les 320; Conservative
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BE523004
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KEYWORDS
SOURCE
ORGANISM
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 486)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   536 GCGACGCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAACGATCCAAC 595
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       Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany
Zoology Bldg., 1735 Nail Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
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Best Local Similarity 100.0%; Pred. No. 6.9e-174;
Matches 334; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="M28F8"
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Plant Functional Genomics Research Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 racaacricirccaaccaccacriricrarccer 345
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                                                                                                                                                                                                Location/Qualifiers
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AV825375.1 GI:19867435
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ò 셤 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

RESULT 2 AV825375 LOCUS

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12149 Lambda-PRL2 Arabidopsis thaliana CDNA clone 156JIT7, mRNA
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(bases 1 to 335)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994).
                                                                                                                                                                                                                                                        /clone lib="Gif-Seeda"
/note="Vector: Lambda ZAPII non-oriented; Physiological
condition: greenhouse plants. tissue_type: Green siliques
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0
Contact: Berthomieu P., Guerrier D., Giraudat J.
Genetique Moleculaire d'Arabidopsis
ISV - UPRO, CNRS
Avenue de la Terrasse,1198 Gif-sur-Yvette Cedex,France
Email: Giraudat@conre-gif.fr.
1.0cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   20.9%; Score 224; DB 14; L
100.0%; Pred. No. 9.6e-113;
ive 0; Mismatches 0;
                                                                                                                                                                /organism="Arabidopsis thaliana"
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Arabidopsis thaliana
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MSU-DOE Plant Research Laboratory
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Seg primer: T7 dye primer.
Location/Qualifiers
1. .335
                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="YAY344"
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Fax: 517-353-9168
Email: 22313tcn@ib
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                                                                    Contact: Benning, C
Debt. of Blochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235068 18-JUL-1994
ATTS3707 Gif-Seeda Arabidopsis thaliana cDNA clone YAY344 5', mRNA
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                                                                                                                                                                               Tel: 517 353 934
Fax: 517 353 934
Fax: 517 353 934
Fax: 517 353 934
Mail: bening@mau.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany
Zoology Bldg, 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 614292937...
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="seed"
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/dev stage="5-13 days after flowering"
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/clone_lib="Arabidopsis developing seed"
/note="Arabidopsis developing seed"
/note="Arabidopsis developing seed; Vector: pBluescript SK-;
/note="Corgan: Developing seed; Vector: pBluescript SK-;
/note="Fcoli; Site_2: XhoII"
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organism="Arabidopsis thaliana"
    (4), 1582-1594 (2000)
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/strain="Columbia"
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    Plant Physiol, 124
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Best Local Similarity 100.
Matches 244; Conservative
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Contact: Chris Town
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Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica oleracea
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 38; Conserv:
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BH450567/c
LOCUS
DEFINITION
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BH511920/c
                                                                                                  BASE COUNT
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// note="vector: lambda zip-Lox; Site_1: Sal; Site_2: Not;
// note="vector: lambda zip-Lox; Site_1: Sal; Site_2: Not;
// note="vector: lambda zip-Lox; Site_1: Sal; Site_2: Not;
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/note="Vector: M13 for .x reads, pBluescript for .b and .g
reads; Site_1: EcoRV; Whole genome shotgun library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA linear GSS 25-FEB-2002 gt27q10.g1 BoBuds01 Brassica oleracea genomic clone gt27g10 5', pundic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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flowering buds. DNA was purified from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 108; DB 14;
llarity 100.0%; Pred. No. 2.7e-48;
Conservative 0; Mismatches 0;
'organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone="gt27g10"
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Location/Qualifiers
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BH741132.1 GI:18875745
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108; Conserv
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Matches 108
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3H741132/c
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Brassica cleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 798)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Wholbished
Oupublished
Other_GSSs; BOHGA14TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH511920 798 bp DNA linear GSS 13-DEC-2001
BOHGA14TF BOHG Brassica oleracea genomic clone BOHGA14, genomic
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using Brassica oleracea TO1000DH3 buds provided by Thome Osborn at the University of Wisconsin. Genomic DNA provided by Pablo Rabinowicz (CSHL) and shotgun library prepared in McCombie Lab."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="BOHG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
210 c 225 g 202 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-3523
Fax: 301-838-0208
Email: cdccwn@rigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 798;
                                                                                                                                                                            Length 586;
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9712 Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT 299
                                                                                                                                                                                                                                                                           262 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%; Score 38; DB 28; I 100.0%; Pred. No. 2.8e-09; iive 0; Mismatches 0;
                                                                                                                                                                          3.5%; Score 38; DB 28; I 100.0%; Pred. No. 2.6e-09; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          41 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coation/Qualifiers
1. 798
/organism="Brassica oleracea"
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/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3712"
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BH450567.1 GI:17636278
GSS.
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BH511920
BH511920.1 GI:17720010
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Gape

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Lycopersicon esculentum Streptophyta; Embryophyta; Tracheophyta; Bubraryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; endicotyledons; core eudicots; asterids; lamida; Solanales; Solanaceae; Solanum; Lycopersicon. [bases 1 to 318]
Ascerzoo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
                                                                                                                                                                                                                                                                                                                                                                                                        318 bp mRNA linear EST 18-MAY-2001 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
/db_xref="taxon:3712"
/clone="BOHTG58"
/clone lib="BO 2 3 KB"
/note="Vector: pH0S1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pH0S1 using BstXI linkers"
1 126 c 160 g 155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                  ch 3.0%; Score 32; DB 28; Length 600; 1 Similarity 100.0%; Pred. No. 5.6e-06; 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 9; Length 318; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande PtoR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,J.
Generation of ESTs from tomato leaf tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1) Score 24; DB 1) Score 24; DB 1) Score 24; DB 1) Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                119 ACTCGAGAGTTAGGTCACAAATCCGACGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                               EST285227 tomato mixed elicito
clone cLET17P7, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="leaf"
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Best Local
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Brassica oleracea
Brassica oleracea
Bukarota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 600)
Town.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
                        Brassica oleracea

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Bukaryota, Magnoliophyta, eudicotyledons, core eudicots, rosids

i (bases II, Brassicales, Brassicaceae, Brassica.

I (bases I Lo 656)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished

Ocher, GSSS: BOGD041TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon.3712"
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
167 c 190 g 157 t
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                              Tel: 301-838-3523
Fax: 301-838-3528
Email: cdownedigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: Sheared ends.
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100.0%; Pred. No. 1.2e-07;
iive 0; Mismatches 0;
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/mol type="genomic DNA"
/strain="TO1000DH3"
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/strain="TO1000DH3"
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BH735681.1 GI:18841076
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Contact: Chris Town
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Fax: 301-838-0208
         Brassica oleracea
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CCESSION TERSION TEYWORDS COURCE ORGANISM

TITLE JOURNAL JOMMENT

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EFERENCE

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/clone lib="tomato mixed elicitor, BTI"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/nots="Tector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Alboi; cLET - Inoculated with a variety of disease response
elicitors: plants exposed to 2,6 dichloroison.cotinic
acid, BTH, jamonic acid, ethylene, fenthion, EIX,
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Virialplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
Lycases 1 to 642
D'Ascenzo,M., He,X., Lyman,J., Holt,I.B., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: DBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5: end with EcoR1 and 3' end with XhoI site."

138 c 128 g 150 t
                                                                                                                                                  642 bp mRNA linear EST 18-MAY-200 EST2838880 tomato mixed elicitor, BII Lycopersicon esculentum cDNA AW041016
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                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 24; DB 9; Length 610;
100.0%; Pred. No. 0.16;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Cornell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761 CCGCCGCCGCTGCTTCGCCGTCGT 784
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Contact: CUG1
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Lycopersicon esculentum

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, asternatophyta; Magnoliophyta, eudicotyledons, core eudicots, asternatophyta; Magnoliophyta, eudicotyledons, cores, by Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Roming, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /close lib="tomato resistant, Cornell"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
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Directionally close Pseudomonas Resistant EST Library.
Directionally closed cDNAs inserted into pBlueScript SK(-) at 5; end with EcoR1 and 3; end with XhoI site."
114 c 110 g 148 t
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D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fulit,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Glovannoni,J.J. and Martin,G.B.
                         EST 18-MAY-2001
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                      AI775374 AI775374 481 bp mRNA linear EST 18-MAY-20
EST256474 tomato resistant, Cornell Lycopersicon esculentum cDNA
clone cLER15G18, mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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LOCUS

ACCESSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

AI484214/c

RESULT 12

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SASE COUNT

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Email: genome-reseges.riken.go.jp,
URL:http://genome.ges.riken.go.jp,
URL:http://genome.ges.riken.go.jp,
Carninci,P.; Nishiyama,Y.; Westover,A., Itoh,M., Nagaoka,S., Sasaki
'N., Okazaki,Y.; Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
'Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokchama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-81: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone_lib="RIKEN full-length enriched, 13 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.rtc.riken.go.jp) further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue type="testis"
dev stage="13 days embryo"
lab_host="DH10B"
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clone="6030466009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/strain="C57BL/6J"
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                                                                         1 (bases 1 to 222)
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                                                                            REFERENCE
                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                               BG129822 670 bp mRNA linear EST 31-JAN-2001 EST475468 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF28K14 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamids, Solanales, Solanaceae, Solanum, Lycopersicon.
1 (bases 1 to 670)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T., Hansen,C., Roming,C. and Tanksley,S. Generation of ESTs from tomato shoot/meristem tissue Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/dlone_lib="tomato shoot/meristem"
okadaic acid, or systemin prior to tissue harvest. site was destroyed during cloning."
144 c 141 g 199 t 1 others
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: https://www.genome.clemson.edu/orders/index.html
Location/Qualifiers
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Pred. No. 0.16;
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/mol_type="mRNA"
/cultivar="TA496"
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0.16;
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clone="cTOF28K14"
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Mus musculus (house mouse)
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0; Gaps Query Match 2.1%; Score 23; DB 10; Length 222; Best Local Similarity 100.0%; Pred. No. 0.41; Matches 23; Conservative 0; Mismatches 0; Indels

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Search completed: February 2, 2004, 05:01:17 Job time : 2490.95 secs

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APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

FILE REFERENCE: GENSET. 031A

CURRENT APPLICATION NUMBER: US 60/091,315

PRIOR APPLICATION NUMBER: US 60/091,315

PRIOR APPLICATION NUMBER: US 60/111,909

PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 140

SOFTWARE: PATENT.

SEQ ID NO: 140

SEQ ID NO: 140

TYPE: DNA
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APPLICANT: Tikco, Suresh
APPLICANT: Tikco, Suresh
APPLICANT: Tikco, Suresh
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
TITLE OF INVENTION: WHERE: US/09/292,034
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
SOFTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 34094
                                             US-09-328-352-1768
US-09-364-206-5
US-09-364-206-5
US-07-853-985A-9
US-07-81-703B-9
US-08-184-236-9
US-08-407-410B-9
US-08-48-500-9
PCT-US91-02370-9
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Pred. No. 4;
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Patent No. 6492343
GENERAL INFORMATION:
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Sequence 8,
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/cgn2 6/ptodata/2/ina/5B_COMB.seg:*
/cgn2 6/ptodata/2/ina/6A COMB.seg:*
/cgn2 6/ptodata/2/ina/6B_COMB.seg:*
/cgn2 6/ptodata/2/ina/PcTUS COMB.seg:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-510-878-3
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US-09-252-991A-6792
US-09-195-940-1
US-09-195-940-1
US-09-553-867A-42
US-09-553-867A-42
US-08-511-280-4
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US-08-444-818-21
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THER INFORMATION: 99-1437-325
                                                                                                                                                                                                                                                           CATION: 97122
HER INFORMATION: 99-1442-224
                                                                "BATURE:
VAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261
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INFORMATION: 5-129-144
                                       GOCATION: 72794
OTHER INFORMATION: 5-124-273
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CATION: 99098
HER INFORMATION: 5-130-257
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ATION: 103806
HER INFORMATION: 5-131-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AME/KEY: allele
OCATION: 108106
THER INFORMATION: 5-135-155
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OCATION: 108471
THER INFORMATION: 5-136-174
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ANNE/KEX: allele
CCCATION: 134362
OTHER INFORMATION: 5-140-348
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CCATION: 99117
HER INFORMATION: 5-130-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AME/KEY: allele
OCATION: 106940
THER INFORMATION: 5-133-375
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OCATION: 108149
WHER INFORMATION: 5-135-198
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OCATION: 108308
THER INFORMATION: 5-135-357
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THER INFORMATION: 5-140-120
                                                                                                                                                                                         AME/KEY: allele
OCATION: 93714
THER INFORMATION: 5-128-60
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LOCATION: 146328
OTHER INFORMATION: 5-143-84
ORGANISM: Homo sapiens
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LOCATION: 134374
THER INFORMATION:
                          NAME/KEY: allele
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NWE/KEY: allele
OCATION: 90819..90865
THER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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OCATION: 90819..90865
FHER INFORWATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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OCATION: 97099. 97145
THER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: 97099..97145
THER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                                LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
                                                                                                                                                                                                                                                                                                                                                          TANENTER: allele
COCALION: 72771...72817
DIHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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LOCATION: 99075. 99121
JTHER INFORMATION: polymorphic fragment 5-130-257 SEQ IDSS
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FERTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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LOCATION: 97130..97177
DTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OCATION: 97130..97177
THER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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JOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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THER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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OCATION: 93690.93736
THER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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                                                : polymorphic base
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                                                                                                                                       : polymorphic
NAME/KEY: allele
ACATION: 146345
TYTER INFORMATION: 5-143-101
EATURE:
                                                                                                                                                                              NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352
                                                                                    NAWE/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24
FEATURE:
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RAME/KEY: allele
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AME/KEY: allele
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THER INFORMATION: n equals a, t, c, or
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OTHER INFORMATION: n equals's, t,
male/KEY: misc_feature
LOCATION: (234220)...(234220)
OTHER INFORMATION: n equals a, t)
                                        LOCATION: (84773)... (84773)

LOCATION: (848773)... (84773)

OTHER INFORMATION: n equals a, t, name of the control (84808)... (84808)

CTHER INFORMATION: n equals a, t, name of the control (84812)... (84812)

CTHER INFORMATION: n equals a, t, name of the control (88120)... (98120)

OTHER INFORMATION: n equals a, t, name of the control (88120)... (98120)

OTHER INFORMATION: n equals a, t, name of the control (88239)... (98239)

OTHER INFORMATION: n equals a, t, name of the control (98266)... (98266)

LOCATION: (98266)... (98266)

OTHER INFORMATION: n equals a, t, name of the control (98343)... (98343)

OTHER INFORMATION: n equals a, t, name of the control (103998)... (103998)

OTHER INFORMATION: n equals a, t, name of the control (103998)... (148948)

OTHER INFORMATION: n equals a, t, name of the control (103988)... (163385)

OTHER INFORMATION: n equals a, t, name of the control (163385)... (163385)

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OTHER INFORMATION: n equals a, t, name of the control (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385)... (163385
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LOCATION: (234814)
LOCATION: (234814)
LOCATION: (234814)
LOCATION: (303781).. (334814)
LOCATION: (303781).. (309398)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc feature
LOCATION: (309418).. (309418)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc feature
LOCATION: (312837).. (312837)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
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LOCATION: (191995)..(191995)
OTHER INPORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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Patent No. 6503729
GARDEAL INFORMATION:
APPLICANT: Bult et al.
ITILE OF INVENTION:
COURTEN NO. 6503729
TITLE OF INVENTION:
Januaschii
FILE REFERENCE: PB275
TITLE OF INVENTION:
Januaschii
FILE REFERENCE: PB275
TITLE OF INVENTION UNMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEG ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO.
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NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
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NAME/KEY: allele
COCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
                                                                                                                                                       NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
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LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
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1.7%; Score 18; DB 4
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
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LOCATION: (28222)...(28222)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695 TCGGAGCTTTCTTCA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
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LOCATION: (1603734)...(1603734)
OTHER INFORMATION: n equals a, t, c, or NAME/KEY: misc feature
LOCATION: (1637998)...(1637998).. ö ò ö ö ö or ö or or ö о Ы ö ö ο OCATION: (855539)..(855539)
THER INFORMATION: n equals a, t, ION: (871619)..(871619) INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (131224). (1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349491). (1349491)
OTHER INFORMATION: n equals a, t)
OTHER INFORMATION: n equals a, t) OCATION: (1119881)...(1119881)

YTHER INFORMATION: n equals a, the construction of the AME/KEY: misc feature OCATION: (779455)..(779455) THER INFORMATION: n equals a, LOCATION: (622708)...(622708)
OTHER INFORMATION: n equals a,
MAME/KEY: misc feature
LOCATION: (657081)...(657081)
OTHER INFORMATION: n equals a, GY: misc_feature ION: (1084830)..(1084830) INFORMATION: n equals a, ON: (1096846)..(1096846) INFORMATION: n equals a, OTHER INFORMATION: n equals a, VAME/KEY: misc feature OCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, OCATION: (713652).. (713652) THER INFORMATION: n equals a, JOCATION: (682442) .. (682442)
JTHER INFORMATION: n equals a, ION: (741684)..(741684) INFORMATION: n equals a, DCATION: (779676)..(779676) THER INFORMATION: n equals a, NAME/KEY: misc feature CCCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, OCATION: (1470091)..(1470091) THER INFORMATION: n equals a, LOCATION: (1602912)..(1602912) OTHER INFORMATION: n equals a, OCATION: (1569020)..(1569020)
THER INFORMATION: n equals a, WAME/KEY: misc feature feature feature feature NAME/KEY: misc_

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 186
LENGTH: 447 ö Gaps Gaps Sequence 2, Application US/08510878
Fatent No. 575771
GENERAL INFORMATION:
APPLICANT: Yu, Fujio
APPLICANT: Kato, Mami
TITLE OF INVENTION: A KANAMYCIN RESISTANCE GENE DERIVED FROM
TITLE OF INVENTION: A ICRORGANISMS OF THE GENUS RHODOCOCCUS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO. Box 747
CTIT: VA
STATE: VA
COUNTRY: USA
ZIP: Z2040-047
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk ô Query Match
1.7%; Score 18; DB 4; Length 1664976;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Query Match 1.6%; Score 17; DB 4; Length 447; Best Local Similarity 100.0%; Pred. No. 47; Matches 17; Conservative 0; Mismatches 0; Indels COMPUTER: IBM PC_compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 Ö ò CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,878
FILING DATE: 03-AUG-1995 | NAME/KEY: misc_feature | DOCATION: (1664854)..(1664855) | OTHER INFORMATION: n equals a, t, c, US-08-916-421B-1 1522815 CAATGICTTTAGCTCCAC 1522798 US-09-328-352-186
. Sequence 186, Application US/09328352
. Patent No. 6562958
. GENERAL INFORMATION: TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-186 170 CAATGTCTTTAGCTCCAC 187 951 TTCATCGTCAATTGCAA 967 326 ricarcarcaridcaa 342 NAME: Weiner, Marc S REGISTRATION NUMBER: 32,181 REFERENCE/DOCKET NUMBER: 12 OTHER INFORMATION: n equals a, FILING DATE: 03-AUG-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: JS-08-510-878-2 ઠ g à

(703) 205-8000

TELEPHONE:

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Query Match
1.6%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches
                                                                            Application US/09252991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6792
                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 CGGCGATTATAGCCGCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 CGGCGATTATAGCCGCC 387
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1.6%;
Best Local Similarity, 100.0%;
Matches 17; Conservative 0
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                                                      -09-252-991A-6878
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US-08-611-280-1/c
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APPLICANT: Yu, Fujio
APPLICANT: Yu, Fujio
APPLICANT: Xato, Mami
TITLE OF INVENTION: MICROORGANISMS OF THE GENUS RHODOCOCCUS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CITT: Fils Church
                                                                                                                                                                                                                                                            DB 1; Length 516;
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 1; Length 748;
                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,878
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wainer Marc 32,181
REGISTRATION NUMBER: 32,181
REGISTRATION NUMBER: 32,181
REGISTRATION NUMBER: 32,181
TELEPHONE: (703) 205-8050
INFORMATION FOR SEQ ID NO: 3: SEQUENCE ABARACTERISTICS:
LENGTH: 746 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 47;
Mismatches
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08510878 Patent No. 5776771
                                                                                                                                                                                                                                                     Query Match 1.6%; Soc
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
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TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                               LENGTH: 516 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-CONT
                                                                                                                                linear
                                                                                                                                                                                           ANTI-SENSE: NO
IS-08-510-878-2
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ACID AND AMINO ACID SEQUENCES
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO GST8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6792, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNDERS: US 60/074,788
FILE REFERENCE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6792
LENGTH: 802
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APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
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47;
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SEQUENCE CHARACTERISTICS
                                     nucleic acid
                                                                              linear
                                                      STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
US-09-195-940-1
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APPLICANT: Matesyyama, Alex
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Canada Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 1353;
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                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
CUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release M:
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
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                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09195940 Patent No. 6258935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              622 GIGGCICAGCAACTICT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930 GIGGCICAGCAACTICT 914
                                                                                                                                                                                                                                                                                                                                                                                  34,688
                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A. REGISTRATION NUMBER: 34,68
REFERENCE/DOCKET NUMBER: 4
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERICS: 1.
SEGUENCE CHARACTERICS: 1.
LENGTH: 1353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linea
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                                                   Gaps
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Grossman, Alex
Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Oncario
COUNTRY: Canada
ZIF: LEN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
              DB 3; Length 1353
                                                   Indels
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100.0%; Pred. No. 46;
ive 0; Mismatches
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REPERENCE/DOCKET NUMBER: A-338A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/195,940
FILING DATE: <UNKNOWN>
            Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-553-867A-42/c
; Sequence 42, Application US/09553867A
; Patent No. 6476188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>
1.6%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; PER
                                                                                                                                                                                                                           Sequence 1, Application US/09562466 Patent No. 6369202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 GIGGCICAGCAACTICI 638
                                                                                            622 GIGGCICAGCAACTICI 638
                                                                                                                               930 dredercadcaacricr 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 17; Conservative
            Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO.
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APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 2; Length 12537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 3758;
45;
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APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Amgen Canada Inc.
6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 45; Matches 17; Conservative 0; Mismatches
                                                                                                                                HYPOTHETICAL: NO
ANTI-SENSE: NO
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: ORGALIC
COUNTRY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOWNTER: IBM PC compatible
TOWNTER: TOWNTER: PCOMPACIBLE
TOWNTER: TOWNTER: PCOMPACIBLE
TOWNTER: TOWNTER: PCOMPACIBLE
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APPLICANT: Matsuyama, Toshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1003 GAGATATACGAGAACA 1019
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                                                        linear
E: DNA (genomic)
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ATTOREY/AGRATION:
NAME: Oleski, Nancy 4.8
REGISTRATION NUMBER: 34,68
REPRENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-611-280-4
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
nucleic acid
IDNESS: single
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CITY: Mississauga
STATE: Ontario
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
US-08-323-477-1
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APPLICANT: Thompson, Stuart
TITLE OF INVENTION: N. MENINGITIDIS RELATED TO THE HEMOLYSIN PAMILY OF TOXINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
                                                                                                                         APPLICANT: Price, Jeffrey
APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
APPLICANT: Takahashi, Joseph S.
TITLE OF INVENTION: A NOWEY L.
TITLE OF INVENTION: A NOWER LOCK GENE AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/553,867A
CURRENT FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 17; DB 4; Length 1960;
100.0%; Pred. No. 46;
cive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Imclone Systems Incorporated : 180 Varick Street New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/920,963
FILING DATE: 28-ULL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08323477 Patent No. 6086896 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           761 CCGCCGCCGCTGCTTCG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ccecceccecrecrice 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 17; Conservative
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us-09-938-842a-1034.oli.rni

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GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
APPLICANT: Grossman, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Amgen Canada Inc.
STREET: 673 Mississauga Road, Suite 303
CITY: Mississauga Road, Suite 303
CITY: Mississauga
STRATE: Ontario
COUNTRY: Canada
ZIP: LSN 636
COMPUTER REAPALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/195,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 1.6%; Score 17; DB 3; Length 12537; Best Local Similarity 100.0%; Pred. No. 44; Matches 17; Conservative 0; Mismatches 0; Indels C
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Gaps

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Search completed: February 2, 2004, 07:58:50 Job time : 89.3221 secs

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ġ.	e 801.301 Seconds	nout alignments) 226 Million cell updates/sec .cacqqtcatcqaaccactca 1071				4869878			JECOMB. seq: * ** PUB. seq: * ** PUB. seq: * JECOMB. seq: * JECOMB. seq: * JECOMB. seq: * JECOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * PUBCOMB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: * FWW_PUB. seq: *	by chance to have a he result being printed, distribution.	Description	Sequence 1034, Ap Sequence 1015, App Sequence 502, App Sequence 257, App Sequence 115, App Sequence 147, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 116, App Sequence 1604, Ap Sequence 1604, Ap Sequence 1604, Ap
Core version 5.1.6 1993 - 2004 Compugen Ltd	g sw model , 03:00:32 / Search	(W1C) 4871 4871	60.0	1822278265 residues		chosen parameters:	0	5 summaries	Applications NA:* /ptodata/1/pubpna/USO7_PUBCOMB.seq:* /ptodata/1/pubpna/USO5_NEW_PUB.seq:* /ptodata/1/pubpna/USO5_NEW_PUB.seq:* /ptodata/1/pubpna/USO5_NEW_PUB.seq:* /ptodata/1/pubpna/USO5_PUBCOMB.seq:* /ptodata/1/pubpna/USO3_NEW_PUB.seq:* /ptodata/1/pubpna/USO3_NEW_PUB.seq:* /ptodata/1/pubpna/USO3_PUBCOMB.seq:* /ptodata/1/pubpna/USO3_PUBCOMB.seq:* /ptodata/1/pubpna/USO3_NEW_PUB.seq:* //ptodata/1/pubpna/USO3_NEW_PUB.seq:*	results predicted to the score of t of the total score	SUMMARIES	US-09-938-842A-1034 US-09-938-842A-1034 US-09-924-035A-502 US-09-770-444-615 US-09-770-656-257 US-10-295-403-147 US-10-369-493-37704 US-10-369-493-37704 US-10-199-550-1 US-10-199-550-1 US-10-245-603A-1 US-09-294-033B-4716 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316
GenCore Copyright (c) 1993	search, using ary 2, 2004,	-09-938-842A-103 71 atggcgacaattcaga	NUC 60.0 , Gapext	eegs,		satisfying	200000000	ng first 45	8 b b c c c c c c c c c c c c c c c c c	number of an or equa	Length DB	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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		IIN N	
	Sequence 5485, Ap Sequence 64, Appl Sequence 216038, Sequence 1216038, Sequence 1216038, Sequence 1216038, Sequence 1317, Appl Sequence 57, Appl Sequence 57, Appl Sequence 17151, Appl Sequence 17151, Appl Sequence 170, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1255, Appl Sequence 1255, Appl Sequence 1255, Appl Sequence 12543, Sequence 132443, Sequence 132443, Sequence 675, Appl Sequence 132443, Sequence 6933, Appl Sequence 132443, Sequence 6933, Appl	TRANSGENIC PLANTS CONTAINING	Length 1071; ndels 0; Gaps 0; CAACTCTAACAGCGTT 60 CAACTCTAACAGCGTT 60 AGACCTTTCCAACTAAT 120
	0 US-09-983-965-5485 US-09-770-444-638 US-10-027-632-216038 US-10-027-632-216038 US-10-027-632-216038 US-10-02-493-2348 US-09-98-842A-337 US-09-98-842A-337 US-09-98-842A-337 US-09-98-842A-337 US-10-10-26-445-59 US-10-10-311-45-99 US-10-10-311-45-99 US-09-98-842A-370 US-09-98-842A-370 US-09-98-842A-370 US-09-98-842A-370 US-09-98-842A-370 US-09-98-842A-370 US-09-96-352-1982 US-09-96-352-1265	US/09938842A -REGULATED GENES OF PLANTS, AND METHODS OF USE 3 US/09/938,842A -24 -24 US 60/227,866 -24 -16 US 60/227,866 -22 -22	Score 1071; DB 10; Pred. No. 0; J. Mismatches 0; I TGAGAAGTTGCAGCAAAAT [
2	5 6 4 4 6 4 4 4 4 5 4 4 4 4 4 4 4 4 4 4	US/05 AMD 33 33 33 1.08 1.08 1.08 1.08 1.08 1.08 1.08 1.08	
	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	action 378A1 378A1 nn nn 1888 378E, 838E, 8180 1900 000 001 001 001 001 01 001 01 01 01 0	100: rvative rvative AATTCAGA AATTCAGA CATCATCA CATCATCA
		74 (100): 0.00 (10	arita onse CGAC TAAC
		RESULT 1 US-09-38-842A-1034 S-09-38-842A-1034 Sequence 1034, Application US/099388 Patent No. US20020160378A1 GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Kreps, Joeff APPLICANT: Wang, Xun APPLICANT: Zhu, Toeff TITLE OF INVENTION STRESS-REGULATE: TITLE OF INVENTION STRESS-REGULATE: TITLE OF INVENTION STRESS-REGULATE: TITLE OF PRIVENTION SAMES. AND METHY FILE SERENCE: SCRIPPI300-3 CURRENT FILING DATE: 2001-08-24 PRIOR PELING DATE: 2001-08-24 PRIOR PELING DATE: 2001-08-24 PRIOR PELING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1034 CEGANISM: Arabidopsis thaliana US-09-938-842A-1034	fatch scal S scal S 1 1 1 61 61
	11111000000000000000000000000000000000	JUT 1 JUT 1 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93 JUD 99-93	Query Nast Ind
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PLANTS, TRANSGENIC PLANTS CONTAINING

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61 GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AAGGITGAAGGAAGAGGAGAAGGATACCGATGCCTGCCACGTGCGGCTAGGATTTTT 300
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361 AACGCTGAGCCGGGATTATAGCCGCCACGGGAACGGTACCGCTCCCGCCATCGCCATG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 TCGGTTAACGCAACCTTAAAAATCCCCGACGACGACGCTCATTCTCATATCGCTGAA 480
421 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGACGCTCATTCTCATATGGGTGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACAACGACAACGATCCAACCTCCG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match. 100.0%; Score 1071; DB 12; Length 1071; Best Local Similarity 100.0%; Pred: No.0; 0; Matches 1071; Conservative 0; Mismatches 0; Indels 0; C
APPLICANT: Wang, Xun.
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLAN:
TITLE OF INVENTION: STRESS-REGULATED GENES OF USB
TITLE OF INVENTION: SAME, AND METHODS OF USB
TITLE OF INVENTION: SAME, AND METHODS OF USB
TITLE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US 60/22, 866
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Arabidopsis thaliana US-09-938-842A-1034
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3-09-938-842A-1034 Sequence 1034, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION: APPLICANT: Harper, Joeff APPLICANT: Kreps, Joel

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960 AATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACA 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    955 TCGTCAATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAG 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895 TCAAGAGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCA 954
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900 AGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACAGGTAGTTCATCGTC
                                                                       161 AGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             835 TTACAAGTIGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTA
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APPLICANT: Slader, Ted
APPLICANT: Blader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Horfman, Neith
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LAllana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
FRIOR PRICATION NUMBER: 05/09/770,444
FRIOR PRICATION NUMBER: 06/178,502
PRIOR APPLICATION NUMBER: 06/178,502
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PRIOR APPLICATION NUMBER: 100/107,502
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PRIOR APPLICATION NUMBER: 100/107,502
PRIOR APPLICATION NUMBER: 100/1
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26.7%; Score 286; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 3.9e-145;
Matches 286; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 615, Application US/09770444 Patent No. US2002023280A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i LOCATION: (1)...(453)
i OTHER INFORMATION: n = A,T,C or G
US-09-770-444-615
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Ledford, Brooke L.
Woesner, Jeffrey P.
Haas, William David
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ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gorlach, Jorn
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                                                                                                                                                                  GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACGGGTAGTTCATCGTCA
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Sequence 502, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Grlach, Jrn
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERRANCE: 2011US
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SEQ ID NO 502
LENGTH: 460
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Best Local Similarity 99.6%; Pred. No. 9.1e-147;
Matches 459; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(460)
OTHER INFORMATION: n = A,T,C or G
S-09-924-035A-502
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106 TCGTCAATTGCAACAACAACGACGCGCACACGCTGAGAGACTTCTCCCTAGAGATATATAGGAG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 GCAAAGATCAAACTCTAAGAGCCGTTGATCTAACCATCATCAACGCGCGTCAGAAACGTCG
                                                                     1015 AAACAAGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 185;
                                                                                                                     46 AAACAAGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: States, red APPLICANT: Davis, Keith R. APPLICANT: Davis, Keith R. APPLICANT: Allen, Keith R. APPLICANT: Allen, Keith R. APPLICANT: Hoffman, Datrick TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: Expressed Sequences of Arabidopsis TITLE OF INVENTION: Analiana FILE REFERENCE: 2031US (PARA-020PRV) CURRENT FILING DATE: 2001-01-26 PRIOR PAPLICATION NUMBER: 60/178,278 PRIOR PILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
17.3%; Score 185; DB 9; I
Best Local Similarity 100.0%; Pred. No. 4.9e-90;
Matches 185; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                           equence 257, Application US/09770696 tent No. US20010044940A1
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Publication No. US20030101481A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      age, Amy
atthew, Abraham V
edford, Brooke L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   u, Yang
kameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                          An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                    Raines, Tracy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 TGATGCCGTCGT
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APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Blatch S.
APPLICANT: Gao, Yongwei
APPLICANT: Gladan, Barry S.
APPLICANT: Ghow, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERBREE: 38-10(5205) B
CURRENT APPLICATION NUMBER: US (10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 37704
LENGTH: 1263
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                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PLANT GENE SEQUENCES I
FILE REFERENCE: MB--0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-22
PRIOR PELING DATE: 1998-09-22
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-2
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 170
LENGTH: 1604
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Publication No. US20030233675A1
GENERAL INFORMATION:
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US-10-369-493-37704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                    Benito, Maria-Ines
Yu, Guo-Liang
Fromm, Mike
                                                                                             Pineda, Omaira
Reuber, Lynne
Jiang, Cai-Zhong
Keddie, James
Zhang, James
rd, Jacqueline
echmann, Jose
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; LOCATION: (143)..(1345)
; OTHER INFORMATION: G802
US-10-295-403-147
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Best Local Similarity
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Best Local Similarity
Matches 18; Conserva
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US-09-294-093B-4716/c
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Pred. No. 20;
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100.0%; Pred. No. 20;
    0; Indels
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CURRENT APPLICATION NUMBER: US/10/199,550
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 09/963,038
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10245603A
Publication No. US20030130187A1
GENERAL INFORMATION:
APPLICANT: REDDY, Police Seshidhar
APPLICANT: TIKOO, Suresh Kumar
APPLICANT: BABIUK, Lorne A.
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REFERENCE: 293102002410
                                                                                                                                                                            Sequence 1, Application US/09963038A
Publication No US20030143200A1
GENERAL INFORMATION:
APPLICANT TIKCO, SULESH K.
TITLE OF INVENTION: PORCINE ADENOVIRUS E1 REGION
FILE REFERENCE: 291102003200
CURRENT APPLICATION NUMBER: US/09/963,038A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
SOFTHARE: FREESE FOR Windows Version 4.0
SEQ ID NO 1
LENGTH: 34094
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100.0%; Pred. No. ...
  0, Mismatches
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Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Porcine Adenovirus Type 3
S-10-199-550-1
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                                       764 CCGCCGCTGCTTCGCCGTCG 783
                                                                               874 cceccecrecircecerce 855
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20; Conservative
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Best Local Similarity
Matches 19; Conserv
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Matches
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APPLICANT: inlight, Raghunath, V. APPLICANT: inlight, Raghunath, V. APPLICANT: Ito, Laura, Y. APPLICANT: Ito, Laura, Y. APPLICANT: Blarman, Bradley, K. APPLICANT: Blarman, Bradley, K. TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REPRENCE: PL-0009 US CURRENT APPLICATION NUMBER: US/09/294,093B CURRENT APPLICATION NUMBER: 06/022,567 PRIOR FILING DATE: April 21, 1996 PRIOR FILING DATE: April 21, 1996 SOFTWARE: PERL PROGRAM.
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) OTHER INFORMATION: Incyte ID No. US20010051335A1 700354854H1

) NAME/KEY: unsure

) LOCATION: 96, 99-100, 198, 205

) OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-4716
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA'LIBRARIES
FILE REFERENCE: 20411-756
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1.8%; Score 19; DB 16;
Best Local Similarity 100.0%; Pred. No..20;
Matches 19; Conservative 0; Mismatches 0
CURRENT FILING DATE: 2002-12-10
PRICR APPLICATION NUMBER: US 09/292,034
PRIOR PLING DATE: 1999-04-14
PRIOR PLLING DATE: 1999-04-15
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FREUSEQ for Windows Version 3.0
LENGTH: 34094
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
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Sequence 30316, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Porcine Adenovirus Type 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21527 AGCAGCGCTTTGTATCCG 21545
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0; Gaps
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION AND DIAGNOSIS OF OVARIAN CANCER
TOWNER OF SEQ ID 1012. 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
SEQ ID NO 1604
LENGTH: 424
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US-09-918-995-34549/c
Sequence 34549, Application US/09918995
Publication No. US20030073623A1
Sequence 18-549, Application US/09918995
Publication No. US20030073623A1
APPLICANT: Hyseq, Inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILLE REFRENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/228,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SSO ID NO 34549
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                      DB 11; Length 364;
63;
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63;
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PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30316
(LENGTH: 364
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1.7%; Score 18;
Best Local Similarity 100.0%; Pred. No.
Matches 18; Conservative 0; Mismatc
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Patent No. US2002052591A1
                                                                                                                                                                                                                                LOCATION: (1).T.(364)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-30316
                                                                                                                                                                                                                                                                                                                                                                                                                                      603 AGCTCTGGCATCATCCAC 620
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Best Local Similarity 100.(
Matches 18; Conservative
                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-34549
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CRGANISM: Homo sapiens
US-09-777-564-1604
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DB 9; Length 424;

1.7%; Score 18;

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1
CURRENT PAPPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FascSEQ for Windows Version 4.0
SEQ ID NO 1604
LENGTH: 424
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63;
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1.7%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches
                           0; Mismatches
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                                                                                                                                                                                                                  Sequence 1604, Application US/10015219
Publication No. US20030008299A1
GENERAL INFORMATION:
                                                                 603 AGCTCTGGCATCATCCAC 620
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CRGANISM: Homo sapiens
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Citle:

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Arabidopsis thaliana (thale cress).
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Erassicales, Brassicaceae, Arabidopsis. AX509034 1677 bp E Sequence 3729 from Patent W00216655: AX509034 AXS09034.1 GI:23390271

ORGANISM

Harper, J.F., Kreps, J., Wang, X. and Zhu, T. Stress-regulated genes of plants, transgenic plants containing REFERENCE AUTHORS TITLE

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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 91554)
1 (bases I to 15554)
1 (bases I to 10554)
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
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1621 GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTA 1677
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Patent: WO 0216655-A 3729 28-FEB-2002;
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ESQATFRVNSASGLTSKWIDSINGTRSTSRNRASRRIKKSEFLIQFGCVTSNPDDLVII
IGATNKPQELDDAVLRRLVKRIYVPLPDSNVRKLLFKTKLKCQFHSLSDGDIDKIVKE
TEĞKLYKLLGYKKIRFISQYTDKRYSGSDLQALCEBRAMMPIRELGANILTIQANKVLN
FSVSQINVEVCLSLKGLINRCVHVTCKISTI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MSFLRGIIDSFSSILNEESKKDPSVSSSSTSSESMNGIDGVPVT
NERTAYKLKGOYPDLAKEEIAKGVRABEWGLHDDALLHYRNAQRIMMEATSTPSPSYIS
SSBKERVARSYREKISHWQNQVSERLQALGVGMSENKRTVAYPSSASVSSTASRYRKTL
SQKTPVARGGVATPRNWKDAAASPRPVVRESGNYYDDKLVEMINTTIVDRSPSYKWDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRFLVESEKDPENMNDKYLRDIILNFMIAGKOTTAALLSWFLYMLCKNPLVQEKIVQE
IRDVTFSHEKTTDVNGFVESINEEALDEMHYLHAALSETLRLYPPVFVDMRCAENDDV
LPDGHRVSKGDNIYYIAYAMGRMTYIWGQDAEEFKPERWLKDGLFQPESPFKFISFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSRFIDPLWKLKWFFNIGSQSKLKKSIATIDKFVYSLITTKRKELAKEQNTVVREDIL
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complement (join (<3414. .3616,3639. .3825,3916. .3965,
4092. .4215,4582. .4712,4769. .4864,4948. .5188,5352.
5506. .5585,5670. .>5980))
complement (join (3414. .3616,3639. .3825,3916. .3965,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="synonym: F17K2.4"
oin(<6429. .6950,7026. .7310,7386. .7724,7806. .8006,
                                                     Complement (join (1002. .112,1208. .1280,1366. .1580,
1655. .1750,1886. .2128,2260. .2388))
/gene="At2g45490"
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9289. .9356,9459. .>9632))
/gene="At2g45520"
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9289. .9356,9459. .9612))
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                                                                                                                                                                             /codom_start=1
/codom_start=1
/product== putative protein kinase"
/protein_id="AAC06151.1"
/db_xref="GI:2979542"
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/gene="At2g45500"
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gene="At2g45510"
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gene="At2g45510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant http://www.igr.org/softlab/glimmerm.htm/glimmerm.html, and GeneSplicer (Mihaela Pertea, and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by ERNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://tp.genome.washington.edu/RM/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(57. .242.335. .747)
gene="At2g45480"
note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="DESKPSVQKFFPEVSDKCLBAAKFSSNRKNDIIARSREWKNNVV
NGAIPHGHTHESDTYLQERGCFRLQVYBTDNBFGBCRRTDGKKWRCSKDVLSGQKYCD
KHMIRGMKKKHFVDTTYNSHBNAGFSFLTVETAVRSVYPCKDGDDQKHSVSWMGITLPR
VSDEKSTSSCSTDTTITDTALRGEDDDESYLSLFSPGV"
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inote="overlap with BAC clone F4L23 (AC002387:1. .1281)."
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/gene="Ar2945450"
/note="8yroows: F77K2.2; contains a protein kinase domain
profile (PDOC00100)"
                                                                                                                                                                                                                                                                                                                                                                                                             9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAC clone F17K2 is from Arabidopsis thaliana chromosome 2 and is near the molecular marker(s) FLS.
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                         Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91854)
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1655. .1750,1886. .2128,2260. .>2388))
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-FBB-2002) The Institute for Genomic Research, 9 Medical Center Dr, Rookville, MD 20850, USA, cdtcwm@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598396. Address all correspondence to:at@tigr.org
Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence
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yroduct="hypothetical protein"
yrotein_id="AAF18607.2"
db_xref="GI:20197053"
                                                                                                                                                                                                                                                                                                                  Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FEB-2002) The Institute
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join(<57. .242,335. .>747)
gene="At2g45480"
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="2"
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                                                                                  (bases 1 to 91854)
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                                     Unpublished
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AUTHORS
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76628 TAAGCTTCTCTATGTCTAAAGAAATGGACGATACGAATAAAACAAGCATCATTAAAGAT 76569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76808 GGTTAAGCGTTTTACGTTTATATGCAACGAAGAATATTGCCATTGTTGGAATGC 76749
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YTSPSPHDSTKQVVEKKKKRKKKREKNATESDGDDSVVEKKKKKRRENGTRFEN
ELLAIDGRSKRKEKKKYWEAKKQKKNKGKTBDTLRENFPKHEDIRFGDVVQAPIKLA
VVPKARKSTLSASQERLRLQAIDAYRSRKGWTARPGVPIPAVMMQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76508 AAAAACATGGGATCCAAAACCTCAAATTTACCAATCAGCCCAAATTATTGATGCTGGCG 76449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76448 TAATGAATGGTATGCTGATGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATTATC 76389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'r anslation="MQSSSSGGDDLEKQQQQQKDKSPQKQSESANESNHITIVVCN
ESSREELVGQTPPEKEVSLSRNGSSHBQCRVCLQPKEEVITBLGGCRGGLAKHRS
IDAMFRIKGSNGCTCQVVANVTPPETOPTINYWWR IDPSYRQERERRGCSSPLW
AFSILIGGLMLDVLISITLGVSALPVNIIOVUNGLGTALRITLEFCYEWSLRRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AAAAACATCGGAATCCAAAACCTCAAATTTACCAATCAGCCCAAATTATTGATGCTGGCG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TITITCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 240
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                                                                                                                                                                      9408. .9427
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complement(9578. .9632)
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9822. .10798
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; Pred. No. 0;
0; Mismatches
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complement(10833. .25573)
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complement (join (<10833.
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1988. .10007
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6388 CCICTGIGGTGGACCCGAITCTGTAATCGGAAAGGTGGAACCCACTTGGTTTAACTTTT 76329	A-	6328 AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCC 76269	8=	6268 GGATCCGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTAATTTTTAATTTTTGAGTG 76209	601 GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG 660 660 660 661 661 661 661 661 661 661	661. AGACTAGGCTCCAGCCCAATTCACATTTCGTTTTGTAGCCTTTTTTTT	CICAGGCCCACAITCACAITITCGITITTGIAGCCITICITITCTGG	721 TECTTACGGTCCCTCTTTCTGGTCGGTCGGTAGTACAAGTAGCTAGTGGTCGTTCAAA.7	88 IGCTIACGGICCCICTITCIGGICGGICGTATGIACAAGIAGCAIAGCIAGIGGITCAAA 76	781 CCGAAACAAGTACCAACCAATCAAAATAAGTTTGAATCGGTTACATTACGTTC 840 6028 CCGAAACAAGTACCAACGAATCAAAATAAGTTTCAATTACATTAAATAACAAGAACAAGTAACAAGAACAAACA	841 AACTIACAATCATTICGATTACTITGATCTGGATTICTAGTTCGGTTTGTATGTTTAATAT 90	5968 AACTTACAALCATTICGATTACCTTGATTICTAGTICGGTTIGTAIGTTAATAT 75909	901 CCGANITGIACAAGTACAAAAAAAAAAAAAAAAAAAAAAAAAAAA	08 CCGGATTGTACAAGTACACAAGTACATAAGTATGCGTATATGTGTATGTGACCGGTTTAATC 7	961 AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTA 1020 11	ATTACCTITITIGGEOGGEOGGEOCCTICATGACCTACATTAATGGGGTCCAACCCCAAGTATG	S ATTAGECTITITICATIGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAAGCTATG 75	1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCATAAAATT 1140 5728 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCATAAAAATT 75669	1141 ATTGAAATCTTTCGAACCATAGAAAAGTTAAATTTGATGAGGATGGAATTTTTGTAC 1200	5668 ATTGAAATCTTTCCAACATAGAAAGTTAATTTGATCAGCAATGGAAATTTTTTTT	1201 AAAGCTAGGTATTTCATTTGGAGTGTACTAGTAACTAGTAAGTA	261 TICTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAAAA	548 TTCTGATTTTGGATTTTGAAGGTTTTCTTAGGTTAAAAAAAA	AAACATTITGTGAAAAAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG	5488 AAAAGAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG 75429	1381 TCCCATAATACTGATAGAAGATAGAATGGAAAGTGATTGTTCACGTGGTACAA 1440	ataataatactigatagaagatagagaatggaaagtgaattigiticacgitggaacaa 7	1441 TOGGAALGGTTCTTTAAAGCTGATCGAACACACACGCGCTGGATGATTTTCCCGCATCAA 1500 	1501 AAAGGSTTGAATACTATTCTCACTTGTTTTCCTGCTCCTATATATA
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Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots;
rosida; eucosida II; Brassicales; Brassicaceae; Arabidopsis

1 (bases 1 to 1660)
Samada, K. Liu,S.X., Sakano, H. L., Toriumi, M., Yu,G., Bowser, L.,
Carninci, P., Chen, H., Cheu, R., Hayashizaki, Y. Ishida, J.,
Lin,G., Miranda, M., Nariesaka, M., Nguyen, M. Palm,C.J., Sakurai,T.,
Satou, M., Seki, M., Shina, P., Southwick, A., Shinozaki, K.,
Lin,G., Miranda,M., Shina, P., Southwick, A., Shinozaki, K.,
Davis,R.W., Ecker, J. R. and Theologis, A.
Arabidopsis Full Length cDnA Clones
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Uns. Bowser, L., Carninci, P., Chen, H., Chen, R.,
Ramai, J., Rim, C., Koesema, E., Lan, B., Lin, J., Maramura, Y.,
Wu,G., Yu,S., Bowser, L., Carninci, P., Chen, H., Kamiya, A.
Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.B.,
Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A.
Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A.
Shinozaki, K., Davis, R.W., Scker, J. R. and J. Unice, Collection and clustering of Rafic Collection and clustering of Rafic Collection and Clustering of Rafic Collection and Clustering of Rafic Collection and Clustering of Rafic Collection and Clustering of Rafic Carninci, Kawai, J., Carninci, P., Carninci, P., Kawai, J., C., Sakin, Sakin, M., Sakin, M., Sakin, W., Sakin, Sakin, W., Sakin, W., Sakin, W., Sakin
         1286 TITITIAGAICATCAAGGCICCIACAGAITICTIAGGGAAIGGITICAGGCTITIGITA 1345
                                                                                                                                                                                                                       1406 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATAGGAAGAATAAAACAAGCATCATTAAAGAT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV056214 1660 bp mRNA linear PLN 18-SEP-2002 Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680)
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Location/Qualifiers
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                                                                                                    1346 GAAATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA
                                                                                                                                                                                     181 TAAGCTTCTCTATGTCTAAAGAAATGGACGATACGAATAAAACAAGCATCATTAAAGAT
                                                                    121 GAAATTGTGTTTATTGCAACAGGTAGAAACATAAACCATAGACAGATGTATCTGAAGAGA
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                                                                                       1561 ACATITAGTAATCTCCTTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCC 1620
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Arabidopsis thaliana shrunken seed protein (SSE1) mRNA, complete
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DKKWNYIILTEAMKAVIRLALFRNSGYKMLLQGGETPNEEKDSNQSESQNRAGNSGRN
LGPHGLGNQNHHNPWNLEGRAMSALSSFGQNARTTTSSTPGWSRRIQHQQAVIEPPMI
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LGWGLLANSKWWGEKSKOVHFGGPEKDELRRRKLIWALYLMRDPFFTKYTRQKLESSQ
KKLELIPLIGPLTEKTVELLEGAQSRYTYISGS"
268 77 9 407 t
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Lin, Y., Sun, L., Nguyen, L.V., Rachubinski, R.A. and Goodman, H.M.
The Pexi6p homolog SSEI and storage organelle formation in
Arabidopsis seeds
Science 284 (5412), 328-330 (1999)
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                                                                                                                                                                                                              9
                                                                                                                                                                        Lin.Y., Sun,L., Nguyen,L.V. and Goodman,H.M.
Direct Submission
Submitted (19-AUG-1998) Molecular Biology, Massachusetts General
Hospital, 50 Blossom Street, Boston, MA 02114, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC
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11.5%; Score 193; DB 8; Length 1483;
Best Local Similarity 99.6%; Pred. No. 3.7e-95;
Matches 243; Conservative 0; Mismatches 1; Indels
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mol_type="mRNA"
culfivar="C24"
db_xref="taxon:3702"
chromosome="2"
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gene="SSE1"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S Muzny, D. Martie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anlen, C., Allen, H., Asoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baddwin, D., Bandamaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P. Brown, M., Carderon, E., Cardenas, V., Cartex, K., Cavazos, I., Ceasar, H., Cener, A., Chenz, C., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Club J., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. La, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Falls, T., Fan, G., Farner, A., Realer, C., Evans, C.A., Falls, T., Fan, G., Farner, A., Realer, C., Evans, C.A., Falls, T., Fan, G., Farner, A., Realer, C., Evans, C.A., Falls, T., Fan, G., Farner, A., Falls, T., Fan, G., Farner, A., Falls, T., Fan, G., Farner, A., Falls, T., Fan, G., Farner, A., Falls, T., Fan, G., Farner, A., Falls, T., Fan, G., Farner, A., Falls, F., Fan, G., Farner, A., Falls, F., Fan, G., Farner, A., Falls, F., Fan, G., Farner, A., Falls, F., Fan, G., Farner, A., Falls, F., Fan, G., Farner, A., Falls, F., Fan, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Farner, G., Fa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACLUBZUU 250957 bp DNA linear HTG-13-MAY-2003
Rattus norvegicus clone CH230-20C16, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tränslation="MATIQKLEEVAGKOQTLRAVDLTIINGVRNVETSRPROVNPTVS'
JEPKAEPVMPSFSMSLAPPSSTGPPLKRASTKDRHTKVEGRGRRIRMPATCAARIFOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rrelghksdgettrwllenaepaitaaggtgtvpalamsvngtlkiptttvadsdmge
Nlmkkkrrrpsnseyidisdavsassglapiattttiqppqalasstvaqqllepqmy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMWAI PSNAMI PTVGAFFLI PQI AGPSNQPQLLAFPAAAASPSSYVAAVQQASTMARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLOVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTTTHTLRDFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTTGGACGTGTAAACGCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCT 60
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                                                                                                                                                    clone="RAFL07-08-P04 (R10678)"
note="This clone is in a modified pBluescript vector
FLC-1) as a BamHI/XhoI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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protein_id="AAL07063.1"
db_xref="GI:15810351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ne,C., Evans,C.A., Falls,T.,
Flagg,N., Forbes,L., Foster,
anta,R., Garcia,A., Garner,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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AC106200.4 GI:30579164
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.1%; Score 102; DB 8; L llarity 100.0%; Pred. No. 1.4e-44; Conservative 0; Mismatches 0;
organism="Arabidopsis thaliana"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 t
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                                                                      xref="taxon:3702"
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                                                                                                                                                                                                                                                                      Columbia"
                                                                                                                                                                                                                                                                                         .1660
gene="At2g45680"
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gene="At2g45680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="At2g45680"
codon_start=1
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Best Local Simil
Matches 102; (
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AC106200/c
LOCUS
DEFINITION
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KEYWORDS
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ORIGIN.
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AUTHORS
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Submitted (13-MAY-2003) Ruman Genome Sequencing Center, Department of Molecular and Human Genetics Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA of Medicine, One Baylor Plaza, Houston, TX 77030, USA of Medicine, One Baylor Plaza, Houston, TX 77030, USA of Maylor Baylor Plaza, Houston, TX 77030, USA of Maylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylor Baylo
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, M., Hornandez, J., Hare, S., Hane, S., Hune, J., Hodgeon, A., Hogues, M., Hollins, B., Howells, S., Huly, S., Hume, J., Iddebird, D., Jackson, A., Jackson, L., Jackson, L., Jang, H., Kang, Z., King, L., Kovar, C., Karpathy, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kolly, S., Mandon, R., Mandou, M., Mandou, R., Mandou, M., Mandou, M., Mandou, M., Mandou, M., Mandou, S., Moleod, M.P., Morell, T.Z., Meenen, E., Mandou, S., Moleod, M.P., Morell, T.Z., Meenen, E., Mandou, S., Moleod, M.P., Morell, T.Z., Meenen, E., Mandou, S., Moleod, M.P., Morell, S., Morels, S., Moleod, M.P., Mortis, S., Morels, S., Moleod, M.P., Mortis, S., Morels, S., Paul, H., Perez, A., Perez, L., Fannkoch, C., Paul, H., Perez, A., Perez, L., Fannkoch, C., Pohndexter, A., Poerez, L., Perez, L., Perez, E., Pully, S., Kedy, T., Rabilly, B., Reilly, M., Ren, Y., Rose, M., Noris, S., Rose, M., Savery, G., Shen, H., Savery, G., Scher, S., Tabor, P., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Taylor, C., Mango, S., Marren, D., Walde, R., Wallson, M., Wallson, M., Walse, R., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson, M., Wallson,
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Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 233323 bases at least 040 Consensus quality: 235744 bases at least 030
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Center: Code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contect: hgsc-help@bcm.tmc.edu
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us-09-938-842a-3729.oli.rge

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC119331 282156 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-291E4, *** SEQUENCING IN PROGRESS
                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bem.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Consensus quality: 238092 bases at least Q20
Estimated insert size: 250301, sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.4%; Score 24; DB 2; Length 250957;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                            1 247058: contig of 247058 bp in length 247058: gap of unknown length 24828: contig of 1070 bp in length 248328: gap of unknown length 250957: contig of 2629 bp in length.
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end_sequence:BH318584"
Complement(243703, .244577)
//note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs end_extension
clone_end:Sp6"
3949. .4624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_end_extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59625 CATAAAATTAAAGTAAATCTTTTT 59602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-20C16"
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245116. .247058
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/note="clone_boundary
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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23911491.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads; assembled using Atlas (http://www.hgsc.bm.tmc.edu/projects/rat/). Each contig described in the feature table below represents; a scaffold in the Atlas ssembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and ordered and separated by sized gaps filled with Ns to the settimated, and separated by sized beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Charez, D., Charde, C., Chan, R., Chen, Y., Chacko, J., Chacke, J., Chacko, J., Chacke, J., Chacko, J., Chacke, J., Drah, M., Chen, J., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, D., Deaderich, J., Charles, M., Flagg, N., Parle, R., Forler, M., Forler, M., Forler, M., Forler, M., Gerker, M., Karath, C., Liu, J., Liu, M., Marker, G., Karath, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Submitted (26-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 282156)
Rat Genome Sequencing Consortium. 2 (bases 1 to 282156) Worley, K.C. Direct Submission Unpublished

Center: Baylor College of Medicine

COMMENT

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Gaps

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linear PAT 11-MAY-2001
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
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                                                                                                                                                                                                                                                                                                                                                                1.4%; Score 23; DB 6; Length 101; 100.0%; Pred No 113;
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Patent: WO 0128540-A 30 26-APR-2001;
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Sequence 30 from Patent W00128540.
AX114618
                                                                                                                         Purvis, I.J. and Mccarthy, L.C.
                                                                                                                                        Therapy of cephalic pain
Patent: WO 0128540-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Seguence 29 from Patent WO0128539
AX114743
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                                                                                                                                                                                                                                               organism="Homo"sapiens"
                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA".
/db_xref="taxon:9606"
15.c :14.g :: 40
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                        Location/Qualifiers
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                       Homo sapiens (human)
Homo sapiens
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AX114743/c
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DEFINITION
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TITLE
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VERSION
KEYWORDS
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                       Center project Information
Center project name: GTVU
Center project name: GTVU
Center clone name: GTVU
Center clone name: GTVI
Center clone name: GTVI
Assembly program: Phrap; version 0.990129
Consensus quality: 253046 bases at least Q40
Consensus quality: 255010 bases at least Q30
Consensus quality: 255010 bases at least Q30
Consensus quality: 25510 bases at least Q30
Consensus quality: 255100 bases; sun-of-contigs estimation
Quality coverage: 6x in Q20 bases; sun-of-contigs estimation
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58459: gap of unknown length
277096: contig of 218637 bp in length
277196: gap of unknown length
278294: contig of 1098 bp in length
278394: gap of unknown length
278394: gap of unknown length
280912: contig of 1518 bp in length
28012: gap of unknown length
282156: contig of 2144 bp in length.
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clone_end:Sp6"
86729 a 49533 c 48244 g 75688 t 21962 others
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0.3;
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                                    Contact: hgsc-help@bcm.tmc.edu
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Sequence 29 from Patent W00128540.
AX114617
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/clone="CH230-291E4"
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/note="clone_boundary
clone_end:T7
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lone_end:Sp6
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complement[209107.
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Best Local Similarity 100.0
Matches 24; Conservative
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                            DB 6; Length 101;
1.3;
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1.4%; Score 23; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels
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1.4%; Score 23; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                            0; Indels
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Diagnostic test for cephalic pain
Patent: WO 0129255-A 29 26-APR-2001,
GLAXO GROUP LIMITED (GB)
LOCATION/Qualifiers
                                                                          Query Match 1.4%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 23; Conservative 0; Mismatches
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Cephalic pain susceptibility marker
Patent: WO 012926-A 28 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Sequence 28 from Patent WO0129256.
AX128089
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Agent for treating cephalic pain
Patent: WO 0128539-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Agent for treating cephalic pain
Patent: WO 0128539-A 30 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Diagnostic test for cephalic pain
Patent: WO 0129255-A 28 26-APR-2001,
GLAXO GROUP LIMITED (GB)
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Sequence 30 from Patent WO0128539.
AX114744
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AX118672
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Test for the diagnosis of diabetes and compounds for the treatment
thereof
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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LOCATION/QUALIFIERS
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Cephalic pain susceptibility marker
Patent: WO 0129256-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Sequence 28 from Patent W00233121.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	11.3 2,700 11.2 2,000 11.1 1,000 11.1 1	99 1.1 4.06 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.	2000 24 111 2352 24 111 2352 24 111 2850 234 111 2925 23 111 2011 24 111 2926 23 111 2926 23	924 standard, DNA; 1677 924; N-2003 (first entry) dopsis thaliana stress	Idopsis thaliana; plant; idopsis thaliana; plant; 2016655-A2; EB-2002, 2001W0-US26685. UG-2001, 2001W8-224866P. UN-2001; 2001US-30011IP; UN-2001; 2001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-3001US-3001IP; UN-2001; Z001US-3001U
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23 1.4 7240 2 23 1.4 7240 2 23 1.4 7240 2 23 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 17646 2 22 1.3 2000 2 22 2.3 1.3 2000 2 22 2.3 1.3 2563 2 24 26 28 28 28 28 28 28 28 28 28 28 28 28 28	20 1.3 2768 2.2 2.1 1.3 2768 2.2 2.2 2.2 1.1 2.2 2.2 2.2 2.2 2.2 2.2	11 19 111 406 2 2 19 111 546 2 4 19 111 546 2 5 19 111 903 2 7 19 111 921 2 11 1 921 2 11 1 921 2	39 19 1.1 2000 24 40 19 1.1 2352 24 42 19 1.1 2357 24 43 19 1.1 2500 23 44 19 1.1 5901 23 45 19 1.1 5901 23	SULT 1 ABZ15924 standard; DNA; 1677 ABZ15924; 21-JAN-2003 (first entry)	Idopsis thaliana; plant; idopsis thaliana; plant; 2016655-A2; EB-2002, 2001W0-US26685. UG-2001, 2001W8-224866P. UN-2001; 2001US-30011IP; UN-2001; 2001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-30011IP; UN-2001; Z001US-3001US-3001IP; UN-2001; Z001US-3001U

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invention relates to identifying a stress condition to which a plant li has been exposed, comprising: contacting nucleic acid representative of expressed polynucleotides the plant cell with an array or probes representative of the plant Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses Claim 144; SEQ ID NO 3729; 577pp + Sequence Listing; English

Cell genome; and the state of expressed polymuclectides in the plant cell genome; and a profile of expressed polymuclectides in the plant cell production of transgence plants, cells and seeds and in producing plants production of transgence plants, cells and seeds and in producing plants with increased tolerance to abject stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office.

Sequence 1677 BP; 508 A; 292 C; 335 G; 542 T; 0 other;

DB 24; Length 1677; 0; Indels ; Score 1677; D; Pred. No. 0; 0; Mismatches 100.0%; Query Match
Best Local Similarity 100.
Matches 1677; Conservative à

GGTTAAGCGTTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 0; Gaps

d ਨੇ g

181 TAAGCTTCTTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 240 TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAGTGAAAGT 300 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAAACAAGCATCATTAAAGAT 240

181

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유 ò g ò 셤

1021 ATTAGETTTTTGGFGGCGCAGCCTTGAGCTACATTAATGGGGTCCAAGTATGG1080 1320 1140 961 AAAGGACGACGATAAGGAGATTTTGGAATCCTGGAAAAGAGGATTATTCCATAGACACTA 1020 1021 ATTAGCTTTTTGGTGGCGCGAGCCTTGTGACCTACATTAATGGGGTCCAACCCCCAAGTATG 1080 1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATT 1140 1141 ATTGAAAATCTTTCCAACGATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTAC 1200 1141 ATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTAC 1200 1561 ACHTTAGTAATCTCCTTGGACGTGTAAAACGATTTTTCCCATTGTATCC 1620 961 AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGAGATTATTCCATAGACACTA 1020 TTTTCTTAGGTTAAAAACAAGTATATTACTAAACAAT 1320 1441 TCGGAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCATCAA 1500 006 780 CCCGGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACGTCGCG-840 840 1621 GCTTTTAACAACTCTCGTCGTCGACCGTCCGTTTTTTCTCTCAGCTATATTTTA 1677 T81 CCCGAAACAAGTACCAACGAATCAAATAAGTTTGAATCGGTTACATCTAGTTACGTTGC 841 BACTIRCHATICGAINACTITICATORATIAN GGCTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATT 1381 TCCCATAATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTGTTCACGTGGTACAA 1261 TTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAAAGAGTATATTACTAAACAAT 1321 AAAAGAAAACAFTFTGTGAAAAGAGAAATAAAGTTFTACTGGACCCCAFTGTACAGATGG 1321 AAAAGAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG 1261 TICTGATTTTGGATTTTGAAGC 721 781 1081 1561 661 721 1381 1441 g 9 ð 8 6 8 6 8 8 6 8 8 8 ઠે 쉼 ठ ු පු 셤 ል ይ ठ ঠ ð

AAA88782 standard; cDNA; 1483 BP AAA88782 RESULT 3

(first entry)

19-FEB-2001

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TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 1465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel shrunken seed gene useful for producing transgenic plants having altered production of food storage reserve material, intracellular transport of storage protein and formation of protein or oil bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTAAGCGTTTTTACTTATGGTTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is that of Arabidopsis thaliana SSE1 (shrunken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An antisense construct is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seed) cDNA, which was isolated from a seedling cDNA library using a partial genomic clone as probe. SSEI encodes a protein (see AAB1918) that, when expressed in a cell of a plant, modifies or alters the production of a food storage reserve material (e.g. protein, lipid or carbohydrate storage reserve, facilitates the intracellular transport of a storage protein, or facilitates the formation of protein or oil bodies. The invention provides a transgent plant (or plant cell, plant tissue, plant organ or plant component) which includes a recombinant SSEI transgene that modifies the production of food storage reserves, thereby
                                                            SSE1; shrunken seed gene; storage reserve; storage protein;
oil body; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1483 BP; 461 A; 268 C; 347 G; 407 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 193; DB 21;
Pred. No. 5.9e-85;
0; Mismatches 1;
                                                                                                                                                                                                                   Location/Qualifiers
122..1225
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modifying desiccation tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 57; 64pp; English
Arabidopsis thaliana SSE1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nutritional value.
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99.6%;
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Best Local Similarity 99.6
Matches 243; Conservative
                                                                                                                                                          Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB19718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin Y;
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directly or indirectly the insulin receptor or Insulin receptor signalling pathway in the manufacture of aimedicament for preventing or treating cephalic pain. Also described is an isolated polymucleotide (II) or protein (III) comprising a polymorphism that causes susceptibility to or protein (III) comprising a polymorphism that is in linkage disequilibrium with the first polymorphism. (I) has antimigraine and vulnerary activities. (I) is useful for treating cephalic pain which may be a cluster headache. (Anonic paroxyman hemicramia, headache associated with vascular disorders, headache associated with substances or their withdrawal (for example drug withdrawal) tension headache and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ly or indirectly insuling receptor or
in the manufacture of medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes the use of an agent (I) that modulates
                                                                                                                                    Insulin receptor; polymorphic site; single nucleotide polymorphism; SNP; migraine; cephalic pain; insulin receptor signalling pathway; antimigraine; vulnerary; cluster headache; chronic paroxysmal hemiora vascular disorder associated headache; withdrawal; tension headache;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represents an insulin receptor oligonucleotide containing a migraine associated polymorphic site, which is used in the exemplification of
                                                                                                                                                                                                                                                                                                 /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 23; DB 22; Length 101; 00.0%; Pred; No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                     Insulin receptor migraine associated polymorphic site #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in particular migraine with or without aura. represents an insulin receptor oligonucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 insulin receptor signaling pathway ir
preventing or treating cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of agent that modulates directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 ACAAGCATCATTAAAGATTAAAT 245
                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 34; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 ACAAGCATCATTAAAGATTAAAT
BP.
                                                                                                                                                                                                                                                                                 replace (51, A)
AAH50475 standard; DNA; 101
                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2000; 2000WO-GB04031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0024713.
99US-0160423.
                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purvis IJ, McCarthy LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-300274/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                   WO200128539-A2
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-0CT-1999;
                                                                21-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                     26-APR-2001
                               AAH50475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 2
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RESULT

1345

120

180

1405

1285

9

Gaps

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1; Indels

Length 1483;

AAH31172/c

migraine; ds.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosis of susceptibility to migraine in individuals comprises the identification of polymorphisms in the insulin receptor gene region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; insulin receptor; antimigraine; cephalic pain; diagnosis; susceptibility; single nucleotide polymorphism; SNP; SNP detection;
                                                                                                                                                                                                                                                                        Human; insulin receptor; diagnosis; cephalic pain; susceptibility; single nucleotide polymorphism; SNP; migraine; SNP detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/standard_name= "Single nucleotide polymorphism"
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1.4%; Score 23; DB 22; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human insulin receptor gene polymorphic site INSBa.
                                                                                                                                                                                                       Human insulin receptor gene polymorphic site INSBa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
replace(51,A)
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AAH31172 standard; DNA; 101 BP.
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                                                                                                                                      (first entry)
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                                                                                                                                      25-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
variation
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                                                                    AAH31172;
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AAH31269/c
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The present sequence is provided in a specification relating to a method for diagnosing susceptibility to cephalic pain in an individual. The method comprises typing in vivo or in a sample from the receptor of individual, the insulin receptor gene region or insulin receptor comparing the protein and thus determining whether the individual is susceptible to caphalic pain. Polymorphisms in the insulin receptor gene that cause susceptibility to cephalic pain have been found. Susceptibility may be diagnosed using a probe, primer or antibody which is capable of detecting an insulin receptor gene region or insulin receptor protein polymorphism. The method is useful for diagnosing susceptibility to migraine, cluster headache, chronic paroxysmal hemicrania, headache associated with substances or their withdrawal, tendion headache, and so on. It is useful for assessing the efficacy of agents in relieving cephalic pain, and can be used to assess the predisposition and/or susceptibility of an individual to the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing susceptibility to cephalic pain such as migraine by typing insulin receptor gene or protein in vivo, or in a biological sample and determining individual's susceptibility to cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         development of diseases mediated by the insulin receptor and in the development of new drug therapies which selectively target one or more allellor variants of the insulin receptor gene. The present sequence corresponds to a polymorphic site and flamking sequences of a single nucleotide polymorphism (SNP) in the human insulin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                           /*tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.4%; Score 23; DB 22; Length 101;
Best Local Similarity 100.0%; Pred. No.:0.69; **
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INSBa polymorphism of human insulin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 ACAAGCATCATTAAAGATTAAAT 245
                                                                    Location/Qualifiers
replace(51,A)
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                                                                                                                                                                                                                                              19-OCT-2000; 2000WO-GB04050.
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                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                     WO200129256-A2
                                      Homo sapiens.
                                                                                                                                                                                                                                                                                   19-OCT-1999;
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                                                                          Key
variation
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Homo sapiens.

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The present invention relates to the use of an agent that modulates directly or indirectly the insulin receptor or insulin receptor or relating pathway in the manufacture of a medicament for preventing or treating cephalic pain. Cephalic pain disorders are generally multifunctional disorder, with a cluster of headache, chronic headache associated with acluster of headache. Chronic headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and in particular migraine with aura or migraine with aura or migraine with aura or migraine with aux or migraine of components of the glucose and lipid metabolism pathways, in particular by manipulation of the insulin receptor. Insulin receptor is an important component in the regulation of the glucose and lipid metabolism pathways. Single nucleotide polymorphisms (SNP) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of agent that modulates directly or indirectly insulin receptor insulin receptor signaling pathway in manufacture of medicament for preventing or treating cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lin receptor gene contribute to susceptibility to cephalic pain, present sequence is INSBa polymorphism of human insulin receptor
Human; insulin receptor; cephalic pain; therapy; headache;
chronic paroxysmal hemicrania; vascular disorder; tension headache;
migraine; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                                 /standard_name= "Single nucleotide polymorphism"
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Pred. No. 0.69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Preα. ν...
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                                                                                                                                                                                                   Location/Qualifiers
replace (51, A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99GB-0024712.
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ABQ72727 standard; DNA; 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin receptor
                                                                                                                                                                                                                                                                                                                                                                    WO200128540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-1999;
19-OCT-1999;
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                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                               variation
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Insulin receptor; polymorphic site; single nucleotide polymorphism; Syny migraths; cephalic pain; insulin receptor signalling pathway; antimigraine; vulnerary; cluster headache; chronic paroxysmal hemicrania; vascular disorder associated headache; withdrawal; tension headache; ds.
                                                                                                                                                                                                                                                                                                                                                                                                         susceptibility to diabetes in an individual. The method of the invention has antidiabetic activity. The method is useful for diagnosing diabetes or susceptibility to diabetes in an individual. Other methods of the invention are is useful for treating diabetes and for treating and preventing diabetes. The present sequence contains a single nucleotide
                                                                                                                                                                                                                                                                                                    Diagnosing diabetes or susceptibility to diabetes in individual by typing insulin receptor gene region or insulin receptor protein in sample obtained from individual
                                                                                                                                                                                                                                                                                                                                                                                              he invention relates to a novel method for diagnosing diabetes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insulin receptor gene exons 14-17 including introns SEQ ID NO:25.
                                                       *tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphism (SNP) present in the human insulin receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23, DB 24; Length 101;
Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; Scc.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 ACAAGCATCATTAAAGATTAAAT 245
                           Location/Qualifiers
replace (51,A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAGCATCATTAAAGATTAAAT 53
                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 31; 61pp; English.
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ID AAH50570 standard; DNA; 7240 BP.
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                                                                                                                                                                                      19-OCT-2000; 2000GB-0025678.
                                                                                                                                                          19-OCT-2001; 2001WO-GB04660.
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                                                                                                                                                                                                                  (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                Hosford D, Purvis 1J;
                                                                                                                                                                                                                                                                           WPI; 2002-500014/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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19-OCT-1999;
                                                                                                                               25-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                           variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH50570;
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McCarthy LC;
                         WPI; 2001-300274/31.
Purvis IJ,
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The present invention describes the use of an agent (I) that modulates directly or indirectly the insulin receptor or insulin receptor to signalling pathway in the manufacture of a medicament for preventing treating cephalic pain. Also described is an isolated polymoclecide (II) or protein (III) comprising a polymorphism that causes susceptibility to cephalic pain, ar aneurally occurring polymorphism that is in linkage disequilibrium with the first polymorphism. (I) has antimigraine and vulnerary activities. (I) has useful for treating cephalic pain which may be a cluster headache, chronic paroxysmal hemicrania, headache associated with vaccular disorders, headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and in particular migraine with or without aura. The present sequence represents exons 14-17 from the insulin receptor gene including introns, which is used in the exemplification of the present invention. Use of agent that modulates directly or indirectly insulin receptor or insulin receptor signaling pathway in the manufacture of medicament for preventing or treating cephalic pain Disclosure; Page 54-57; 58pp; English.

Seguence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;

ô Gaps ö 1.4%; Score 23; DB 22; Length 7240; 100.0%; Pred. No. 0.56; tive 0; Mismatches 0; Indels 0 Query Match Best Local Similarity 100. Matches 23, Conservative

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AH31170/c ESULT 9

AAH31170 standard; DNA; 7240 BP AAH31170;

(first entry) 25-JUL-2001 Human insulin receptor gene, exons 14 to 17.

Human; insulin receptor; diagnosis; cephalic pain; susceptibility; single nucleotide polymorphism; SNP; migraine; SNP detection; ds.

Homo sapiens

WO200129255-A2

26-APR-2001

19-OCT-2000; 2000WO-GB04024

99GB-0024717. 19-OCT-1999;

(GLAX) GLAXO GROUP LTD

Purvis IJ, McCarthy LC;

WPI; 2001-328499/34

Diagnosis of susceptibility to migraine in individuals comprises the identification of polymorphisms in the insulin receptor gene region

Disclosure; Page 38-41; 41pp; English

The present sequence is provided in a specification relating to a method of diagnosing susceptibility to cephalic pain. Polymorphisms

ů cephalic pain, particularly to migraine. The method comprises typing a region of the insulin receptor gene or insulin receptor protein of an individual. A susceptibility to cephalic pain may be diagnosed using a probe, primer or antibody which is capable of detecting a polymorphism in an insulin receptor gene region or the insulin receptor protein. in the insulin receptor gene have been found to cause susceptibility 88888888888

Seguence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;

Gapa . 0 Score 23; DB 22; Length 7240; Pred. No. 0.56; 0; Indels 1.4%; Scor. 100.0%; Pred. No. v... 23; Conservative Similarity Query Match Local Matches

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RESULT 10 AAH31267/c

AAH31267 standard; DNA; 7240 BP

AAH31267;

(first entry) 25-JUL-2001

Human insulin receptor gene from exon 14 to 17.

Human, insulin receptor; antimigraine; cephalic pain; diagnosis; susceptibility; single nucleotide polymorphism; SNP; SNP detection; migraine; ds.

WO200129256-A2 Homo sapiens.

6-APR-2001

19-OCT-2000; 2000WO-GB04050.

19-OCT-1999; 99GB-0024717.

(GLAX) GLAXO GROUP LTD

Purvis IJ, McCarthy LC;

WPI; 2001-316247/33

Diagnosing susceptibility to cephalic pain such as migraine by typing insulin receptor gene or protein in vivo, or in a biological sample and determining individual's susceptibility to cephalic pain

Disclosure; Page 43-46; 46pp; English.

The present sequence is provided in a specification relating to a method for diagnosing susceptibility to cephalic pain in an individual. The method comprises typing in vivo or in a sample from the reserved comprises typing in vivo or in a sample from the individual, the insulin receptor gene region or insulin receptor or protein and thus determining whether the individual is susceptible to cephalic pain. Polymorphisms in the insulin receptor gene that cause susceptibility to cause susceptibility to cephalic pain have been found. Susceptibility and deterting a probe, primer or antibody which is capable of detecting an insulin receptor gene region or insulin receptor protein polymorphism. The method is useful for diagnosing susceptibility to migraine, cluster headache, chronic paroxysmal hemicrania, headache associated with substances or their withdrawal, tension headache, and so on. It is useful for assessing the efficacy of agents in relieving cephalic pain, and can be used to assess the ability of agents to modulate insulin the predisposition and/or susceptibility of an individual to the insulin receptor and in the predisposition and/or susceptibility development of diseases mediated by the ö

development of new drug therapies which selectively target one or more allelic variants of the insulin receptor gene.

Sequence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;

Gaps

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Score 23, DB 22; Length 7240; Pred. No. 0.56; 0; Mismatches 0; Indels

1.4%; Scc... 100.0%; Pre

Local Similarity

Query Match

23;

Matches

AAD04467 standard; DNA; 7240

D04467/c

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he invention relates to a novel method for diagnosing diabetes or susceptibility to diabetes in an individual. The method of the invention as antidiabetic activity. The method is useful for diagnosing diabetes or susceptibility to diabetes in an individual: other methods of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disorder, inflammation, angiogenic diseases; AIDS;
acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; cancer; tumour; hyperproliferative disorder;
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention are is useful for treating diabetes and for treating and preventing diabetes. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein gene 381 genomic fragment HE2CA60, SEQ ID NO:1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                typing insulin receptor gene region or insulin receptor protein sample obtained from individual
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    Indels
                                                                                                                                                                                                                                                                                                                                   Human; insulin; receptor; diabetes; antidiabetic; ds
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  Mismatches
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Pred. No.
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                                                                           5056 acaaccarcarraaacarraaar 5034
                                       223 ACAAGCATCATTAAAGATTAAAT 245
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100.0%; Pre-
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                                                                                                                                                                           ABQ72725 standard; DNA; 7240
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                                                                                                                                                                                                                                                                                              Human insulin receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2000; 2000GB-0025678
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXO GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purvis IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-500014/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   40200233121-A2.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens,
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                                                                                                                                                                                                                                                        09-SEP-2002
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23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosford D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ74645;
                                                                                                                                                                                                                   ABQ72725
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin receptor gene contribute to susceptibility to cephalic pain. The present sequence is complete sequence from exon 14 to 17 of human insulin receptor gene. SNP in this sequence contributes to susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the use of an agent that modulates directly or indirectly the insulin receptor or insulin receptor signalling pathway in the manufacture of a medicament for preventing or treating cephalic pain. Gebhalic pain disorders are generally multifunctional disorder, with a cluster of headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and in particular migraine with aura or migraine without aura. The treatment of cephalic pain and migraine involves manipulation of components of the glucose and lipid metabolism pathways, in particular by manipulation of the insulin receptor. Insulin receptor is an important component in the regulation of the glucose and lipid metabolism pathways. Single nucleotide polymorphisms (SNP) in the
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Human; insulin receptor; cephalic pain; therapy; headache; chronic paroxysmal hemicrania; vascular disorder; tension headache; migraine; single nucleotide polymorphism; SNP; ds.

Human insulin receptor DNA (from exons 14 to 17).

04-JUL-2001

AAD04467;

Use of agent that modulates directly or indirectly insulin receptor insulin receptor signaling pathway in manufacture of medicament for preventing or treating cephalic pain

99GB-0024712.

Purvis IJ, McCarthy LC; WPI; 2001-290815/30

(GLAX) GLAXO 19-0CT-1999; 19-0CT-1999;

19-OCT-2000; 2000WO-GB04051

WO200128540-A2

26-APR-2001

Homo sapiens.

Disclosure, Page 42-45, 46pp, English.

DB 22; Length 7240; 0.56;

1.4%; Score 23; 100.0%; Pred. No.

Query Match Best Local Similarity

Sequence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;

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ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode. ABZ73698-ABZ73698 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins in drug screening and recombinant the use of the secreted proteins in drug screening and recombinant. Covectors and host cells comprising a nucleic acid of the invention. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell migration, prohormone activation and neurotransmitter activity. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and modulators of protein crivity are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, AIDS (acquired immunodeficiency syndrome), hepathtis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromsome acids and and acids the invention may be used for chromsome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and as molecular weight markers. The present sequence represents a human secreted protein genomic fragment referred to in the disclosure of the
drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human secreted proteins and nucleic acids, useful for detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene; ds; protein therapy; immediate hypersensitivity disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 2382-2387; 2474pp; English.
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ABT17023 standard; DNA; 17646 BP.
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
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Best Local Similarity
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BT17023/
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allergic disorder; asthmatic disorder; gene therapy; secreted protein; hay fever; allergic conjunctivitis; allergic chinitis; binding partner identification; chromosome identification; aradiation hybrid mappling; long-range restriction mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of human secreted proteins and nucleic acids for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, e.g. asthma, hay fever, or allergic
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0; Indels 0
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
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Matches 22; Conservative
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                                                                                                                                                                                                                                                           WO200277188-A2.
                                                                                                                                                                                     Homo sapiens.
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WO200277186-A2

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Gaps

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DB 25; Length 17646;

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1.3%; Sco... 100.0%; Pred. No. 0; Mismatches

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(HUMA-) HUMAN GENOME SCI INC.
                                                                                      27-MAR-2001, 2001US-278650P.
12-SEP-2001, 2001US-0950082.
12-SEP-2001, 2001US-0950083.
                                            26-MAR-2002; 2002WO-US09188
                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
03-OCT-2002
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WPI,, 2003-040583/03.
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New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGCACI9), useful for preventing, treating or diagnosing e.g. ALIDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or west Nile fever

Disclosure; Page 2326-2330; 2423pp; English.

The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treatment ameliacrating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antibagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other and prevention of: a cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or unogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid architis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Sequence 17646 BP; 5370 A; 3099 C; 3561 G; 5616 T; 0 other;

Gaps ô Query Match
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0;

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Search completed: February 2, 2004, 03:13:29
Job time : 496.761 secs

8.9 278 29 BZ377781 8.9 347 9 AV521636 6.0 486 9 AV825375 5.1 378 10 BE523004	4.9 146 26 BH617024 2.4 600 29 CC459772 1.6 825 28 BH491162 1.3 207 29 AL764163 1.3 162 28 AQ055392 1.3 178 10 BE933474	1.3 258 10 BF703799 1.3 269 14 CB477075 1.3 310 9 AA224031 1.3 318 9 AW480642 1.3 329 9 AW358594 1.3 330 9 AA224071	1.3 365 9 AI466455 1.3 391 14 CA940873 1.3 406 10 BF449231	1.3 413 10 BE207343 1.3 424 9 AI035951 1.3 440 10 BF707341 1.3 440 10 BE25542	1.3 445 9 AU184321 1.3 455 9 AU184443 1.3 476 10 BF707342 1.3 488 13 BX281427	21 1.3 521 10 BF704377 BF704377 MAS5154 21 1.3 551 9 AM655154 AM655154 AM655154 AM655154 AM655154 AM655154 AM75779 MA 21 1.3 554 12 BM384056 BM384056 U.RDM1- BM384056 U.RDM1- 21 1.3 594 12 BM384056 U.RDM1- BG539984 60539984 6053984 6053984 21 1.3 637 10 BR252939 601117527 BR254600 601113840 21 1.3 663 28 B55012 BS5012 CB309574 AGBNCOURT 21 1.3 707 13 B0134910 B0194940 U.RCML-	1.3 711 10 BE251436 1.3 728 10 BB610568 ALIGNMENTS	a TDNA inear	Burmatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicaejs Brassicaceae; Arabidopsis. 1 (bases I to 317) Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Ueske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.	ratory (SIGNAL) udies , CA 92037, USA	Pax: 858 558 6379
						ш ш ш ш ш ш ш ш ф ф ф ф ш ф Б Ф С В Ф О II И Ш		BEG62927 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM	REFERENCE	Į.	
υ	00 0	. 0 (υυ υ	υ Ω	NES CENTRAL CONTRACTOR	REF A	OO GOO	
5.1.6 Compugen Ltd.	Search time 1880.05 Seconds (without alignments) (0504.671 Million cell undates/sec	cta 1677	dues	rs: 45562784				,	results predicted by chance to have a to the score of the result being printed, of the total score distribution.	Description BZ66297 SALK 0264 AL761108 Arabidops BH612074 SALK 0321	
GenCore version 5.1 Copyright (c) 1993 - 2004 Com	M nucleic - nucleic search, using sw model tun on: Pebruary 2, 2004, 00:53:06; Se (with	itle: US-09-938-842A-3729 Perfect score: 1677 Sequence: 1 ggttaagcgttttacttatg Scoring table: OLIGO NUC Gapon 60.0 Gapest 60.0	hed: 22781392 segs, 1215223	<pre>/ord size : 0 /oral number of hits satisfying chosen parameter</pre>	<pre>finimum DB seq length: 0 faximum DB seq length: 2000000000 ost-processing: Listing first 45 summaries</pre>		04004006	18: em_gss_inv: 19: em_gss_inv: 20: em_gss_pln:* 21: em_gss_fun:* 23: em_gss_mam:* 24: em_gss_mus:* 25: em_gss_pro:* 26: em_gss_pro:* 26: em_gss_pro:*	o: June 1: 1: 1: 25	Secult Query No. Score Match Length DB ID 1 271 16.2 317 29 BZ66297 2 245 14.6 267 29 AL761108 C 3 164 9.8 232 28 BH612074	4 164 9.8 233 28

FEATURES

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/clone 11b="Arabidopsis thaliana T-DNA insertion lines" |
/clone | PCR was performed on DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion Sequences displaying significant processed for submission. T-DNA derived sequence were processed for submission. T-DNA derived sequences were
                       Direct Submission
Submitted (17-UN-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (17-UN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNa. It
indicates an insertion within the locus defined by clone f418. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpir-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 AGTIGGIGGCIGCGAAAATTACAACATTATCCCTCTGIGGIGGACCCGAATCTGTAATCG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 ACGTTATCGCCAATATTTTGATTTTTGAGTGGTAGGAATGGTGGGGTCGAATAGTTGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 GAAAAGGTGGAACCCACTTGGTTTAACTTTTAAGCCTAAAAGGTTACTACCGGTTTGACC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 GAAAAGGTGGAACCCACTTGGTTTTAACTTTTAAGCCTAAAAGGTTACTACGGTTTGACC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570 ACGTTATCGCCAATATTTTGATTTTTGAGTGGGTAGGGAATGGTGGGGTCGAATAGTTGG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 AGTTGGTGGCTGGCTAAAATTACAACATTATCCCTCTGTGGTGGACCGGAATCTGTAATCG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/clone="GK-205F06-014511"
/clone_lib="Arabidopsis_thaliana_T-DNA_insertion_lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.6%; Score 245; DB 29; Length 2
Best Local Similarity 100.0%; Pred. No. 3.2e-113;
Matches 245; Conservative 0, Mismatches 0; Indels
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Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                        VERSION BH612074.1 GI:18059525
KEYWORDS GSS
SOURCE Arabidopsis thallana (thale cress)
ORGANISM Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_D!
/strain="Columbia 0"
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                                 TITLE
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BH612074/c
   AUTHORS
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                                                                                                                                                                                                                    THE WORK
                                                                                                                                                                                                                                                     との問題を持ち
                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1407 GAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAATGGTTCTTTAAAGCTCATCG 1466
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                                                                                                                                                                                                                                                                                                                                          /clone="SALK C26421.45.45.x"
/clone=lb="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana TDNA interformed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

75 c 19 105 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 TITICCTGCTCCTATATATATATCCTGACGAGTCACATTTAGTAATCTCCTTGGACGTGT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
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                              This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAATGGTTCTTTAAAGCTCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                       'organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
16.2%; Score 271; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 271; Conservative 0; Mismatches
                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                     db_xref="taxon:3702"
                                                                TDNA. ...
At2945680.
Class. TDNA tagged.
Location/Qualifiers
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Email: ecker@salk.edu
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1467

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BASE COUNT

87

1527

207

267

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS

RESULT 2 AL761108

core eudicots; rosids

(bases 1 to 232)
 (bane, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P. Zimmernan, J. and Ecker, J. R.

REFERENCE - AUTHORS

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B., A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished

(bases 1 to 267)

JOURNAL REFERENCE

JOURNAL REFERENCE

AUTHORS REFERENCE

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.

1 (bases 1 to 278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AGCTICTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 AGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTA 129
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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                                                This is single pass sequence recovered from the left border of
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Bolological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Eax: 858 453 4379
Bmail: ecker@salk.edu
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Arabidopsis thaliana
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/strain="Columbia 0"
                                                                        TDNA.
Class: TDNA tagged.
Location/Qualifiers
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                ecker@salk.edu
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1 (bases I to 233)
Alonso,J.M., Leises,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Bcker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Unpublished
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/clone="SALK 032102"
/clone="SALK 032102"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines and totes" PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

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                                                                                                    Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
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10010 N. Torrey Panes Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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/mol type="genomic DNA"
/strain="Columbia 0"
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Sequence-Indexed Library
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Matches 164; Conservative
                                                                        Unpublished
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Query Match

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FIREM Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4380

Eax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp

An Arabidopsis full-langth cDNA library was.constructed essentially as reported previously (Seki et al., 1998).cDNA-cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI: This clone is in a modified pBluescript vector. Please visit our web eite (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
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Marayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Madnoliophyta, eudicotyledoms, core eudicots; rosids
; eurosids II; Brassicales, Brassicacee, Arabidopsis.
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itch,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
                                                                                                                                                                                                               241 GGTTAAGCGTTTTACTTTATGGTTTTATGCAACGGAAGAATATTGCCATTGTTGGAATGC 182
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|mol_tvne="mpwx".
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          Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                            121 GAAATTGTGTTTATTGCAACAGGTAGAGA 149
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db.xref="taxon:3702"
/clone="RAFL07-08-P04"
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                                               2.8e-64;
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Plant Functional Genomics Research Group
              8.9%; Score 149; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRNA
                                               Best Local Similarity 100:08; Pred No. 2:8
Matches 149; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GAAATTGTGTTTATTGCAACAGGTAGAGA 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                        61
              Query Match
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DEFINITION
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AV825375
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/mol_type="genomic DNA"
/strain="columbia on"
/db_xref="taxon:3702"
/dlone="SALK_IO6185.39.30.x"
/clone="SALK_IO6185.39.30.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana prote="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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AV521636 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone AP263b12F 3', mRNA sequence.
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
i chases II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 347)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of CDNA in Arabidopsis thaliana: Generation of I2,028 non-redundant expressed sequence tags from normalized and size-selected CDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="ARZ63b12F"
/tisoue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1588 ACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTCGTCGTCATCT 1647
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 ACGCCGTTAAAACGATTCTTTCCCATTGTATCCCCTTTTAACAACTCTCGTCGTCATCTC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1528 TITCCIGCTCCTAIATATATATCTGACGAGTCACAITTAGTAAICTCCTIGGACGTGTA
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 150; DB 29;
Pred. No. 8.7e-65;
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/mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1648 CACCGTCCGTTTTCTCTCAGCTATATTTTA 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 CACCGTCCGTTTTCTCTCAGCTATATTTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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AV521636.1 GI:8681163
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69
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Best Local Similarity 100.
Matches, 150, Conservative
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AV521636/c
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Varidiplantae, streptophyta; core eudicots; core eudicots; resids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Agnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:3702"
/clone="SALK 038853"
/clone="SALK 038853"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 44 c 27 g 42 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1596 AAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTCGTCGTCATCTCCACCGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is single pass sequence recovered from the left border TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                              Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Ga., C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., S., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.9%; Score 82; DB 28; Length 146; 100.0%; Pred. No. 4e-30; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 888 558 658 678
Fax: Espe 558 658 640
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana"
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/mol_type="genomic DNA"
/strain="Columbia 0"
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  BH617024.1 GI:18427119
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 378)
Mhite,J.a., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
Mhite,J.a., Todd,J., Newman,T., Focks,N., and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bening@men.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 173 Nail Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH617024 146 bp DNA linear GSS 30-JAN-2002 SALK 035853 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_035853, genomic survey sequence. BH617024
                                                                                                                                                                                      BES23004 378 bp mRNA linear EST 19-MAR-2001 M31B6STM Arabidopsis developing seed Arabidopsis thaliana cDNA clone M31B6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoR1; Site_2: XhoII"
97 c 81 g 92 t
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1637 GICGICATCICCACCGICCGITITICICICAGCIAIATITIA 1677
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/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                           GTCGTCATCTCCACCGTTTTTCTCTCAGCTATATTTTA
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/mol_type="mRNA"
strain="Columbia"
/db_xref="raxon:3702"
/clone="M31B6"
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BES23004.1 GI:9780982
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Matches 85; Conservative
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Fax: 517 353 9334
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Maroliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 825)
1 (bases 1 to 825)
Whole genome shotgun sequencing of Brassica oleracea
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH493162 825 bp DNA linear GSS 13-DEC-2001
BCGOH91TR BOGO Brassica oleracea genomic clone BOGOH91, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1702"
/clone="SALK 133376.34.05.x"
/clone="Local part of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the cont
                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torsty Phines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 ×1752
Fax: 858 558 6379
Email: ecker©salk edu
This is single pass sequence recovered from the left border of
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Sequence-Indexed Library of Insertion Mutations in the
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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2.4%; Score 40; DB 29; I
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 40; Conservative 0; Mismatches 0;
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Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
/strain="mol000bH3"
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/clone="BOGOH91"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'mol_type="genomic_DNA"
'strain="Columbia_0"
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/clone_lib="BOGO"
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TIGR
                                                                                                                                                                                                                                                                                                                                                                                       Class: TDNA tagged
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BH493162
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RESULT 11

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FEATURES

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Li, Y., Caseo, M., Strizhov, N. and Weisshaar, B.

Direct Submission

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Succhtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F4H6. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat.project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgq.ak/GABI-Kat/.

Location/Qualifiers
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL764163 207 bp DNA linear GSS 18-JUN-2002
Arabidopsis thaliana T-DNA flanking sequence GK-122806-012551,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                                                           Gaps
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers' 174 c 137 g 222 t
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                                                                                                                                                                               1.6%; Score 26; DB 28; Length 825;
100.0%; Pred. No. 0.15;
.ive 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
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100.0%; Pred. No.
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Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-HT0887-250 800-012-d07&t3=2000-68-25&t4=1) Seq primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 154. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Adult"
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                              Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the FAPESP/LICR Human Cancer Genome
                        Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R. Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H. Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 258)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rud Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Normalization and subtraction: two approaches to facilitate gene
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MI-P-E4-abq-h-11-1-UM.81 MI-P-E4 Sus scrofa cDNA clone
MI-P-E4-abq-h-11-1-UM 3', mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
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97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Emal: asimpson@ludwig.org.br
This sequence was derived from
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1 (Dases 1 to 162)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Base, S., Linher, K., Simon, M. and Venter, J.C., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Building (1998)

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ordedame@cigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                       AQO55392 11-HSP Homo sapiens genomic clone 2344P6
   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   0; Indela
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Pred. No. 50;
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db_xref="taxon:9606"
clone="2344P6"
                                                         1308 ATTACTAAACAATAAAAGAAAA 1329
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Tel: 5152944252
Fax: 5152944252
Fax: 5152944261
Email: ckrugale@iastate.edu
Email: ckrugale@iastate.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand coNA and therefore this may represent a bonafile poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized embryo at gestational day 14 library CDNA tibrary
Preparation: RJ Woods, JA Green, RS Prather 5142 Animal Science
Research Center, Department of Animal Science, University of
Missouri-Columbia, 65211 Clone distribution: clones will be
available through Research Genetics (www.resgen.com)
Seq primer: MJ3 Forward
POLYA-Yes.
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/lab host="mHIDB (Life Technologies)"
/lab host="mHIDB (Life Technologies)"
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/lab host="mHIDB (Life Technologies)"
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/note="Vector: pTT3D-Pac (Pharmacia) with a modified
/note="Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker: Site 1: Not 1; Site 2: BcoRI; The MI-P-E4
library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at
rkf Lip=MI-P-E4
TAG LIB=MI-P-E4
TAG LIB=MI-P-E4
TAG TISSUE==mbryo at gestational day 14
Molecular Genetics Laboratory, Department of Animal Science
                                      Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
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1. .258
/organism="Sus scrofa"
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'strain="crossbreed"
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Ouery Match 1.3%; Score 21; DB 10; Length 258; Best Local Similarity 100.0%; Pred. No. 51; Matches 21; Conservative 0; Mismatches 0; Indels

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Search completed: February 2, 2004, 05:01:24 Job time : 3888.05 secs

us-09-938-842a-3729.oli.rni

Sequence

Sequence

Sequence Sequence

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Sequence 6, Application US/08340539A

Sequence 6, Application US/08340539A

Patent No. 5808025

GENERAL INFORMATION:

APPLICANT: Tedder, Thomas F.

APPLICANT: Tedder, Thomas F.

APPLICANT: Tedder, Thomas F.

TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 28

CORRESPONDRICE ADDRESS:

ADDRESSER: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

CONTRY: USA
                                                                                                                                                                                                                                                         Sequence 1'
Sequence 1'
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIONS
SOFTWAREN
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539A
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/459
FILING DATE: 25-JAN-193
ATTONEY/AGENT INFORMATION:
NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: 38,479
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEFRAX: 212-596-9090
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US-09-620-3120-1731
US-09-382-256-17
US-09-392-256-17
US-09-392-115-17
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(c) 1993 - 2004 Compugen Ltd.
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Geguence 6, Application US/08461592B

TITLE OF INVENTION: ELOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11

CORRESTOR SEQUENCES: 12

STATES ADDRESSE: Waingarten, Schurgin, Gagnebin & Hayes

STILES MADESSE: Waingarten, Schurgin, Gagnebin & Hayes

STILES MADESSE: Waingarten, Schurgin, Gagnebin & Hayes

GITY: Boston

CONTRIS: Name of Computable

CONTRIS: Name Press PROW disk

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SECURITY NAMER: US 08/140,539

FILING DATE 16 MON-1994

PRIOR APPLICATION NAMER: US 08/140,539

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PARTICULARY: 1917.713 Seq. 14.

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APPLICANT: Stockinger, Eric
APPLICANT: Stockinger, Eric
APPLICANT: Garlo-Outcosen, Kirsten
APPLICANT: Garlo-Outcosen, Kirsten
APPLICANT: Zarka, Daniel
APPLICANT: Zarka, Daniel
APPLICANT: Zarka, Daniel
APPLICANT: Jang, Cai-Zhong
TITLE OF INTON: Plant Having Altered Environmental Stress Tolerance
FILE REFERENCE: 19117.713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
GURRENT FILING DATE: 1998-11-23
PRIOR FILING DATE: 1998-09-04
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Patent No. 6268548
GENERAL INFORMATION:
APPLICANT: Blthon, Thomas E
APPLICANT: Lund, Adrian A
APPLICANT: Bhattramakki, Dinakar
APPLICANT: Rhattramakki, Dinakar
APPLICANT: Rhoads, David M.
TITLE OF INVENTION: Isolation and Characterization of Heat Shock Protein
FILE REFERENCE: UNVNS2819
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Best Local Similarity 100.0%; Pred. No. 27,
Matches 18; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR PELICATION NUMBER: US 09/018,235
PRIOR PELICATION NUMBER: US 09/018,235
PRIOR PILING DATE: 1998-02-03
PRIOR PRILING DATE: 1998-02-03
PRIOR PELICATION NUMBER: US 09/018,227
PRIOR PELING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 68
LENGTH: BROTH VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68, Application US/09198119C
Patent No. 6417428
GENERAL INFORMATION:
GRPICANT: Thomashow, Michael
                                                                                                                                                                                                                               1364 CCCCATTGTACAGATGGT 1381
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OTHER INFORMATION: boCBF5 gene
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ORGANISM: Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                          ESULT 5
JS-09-198-119C-68/c
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US-09-249-180-1/c
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Gape
CURRENT APPLICATION NUMBER: US/09/249,180
CURRENT FILING DATE: 1999-02-12
EARLIER APPLICAND NUMBER: 60/076/014
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Created in Patentin Ver. 2.0, Edited in WordPerfect 6.1
LENGTH: 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 18; DB 3; Length 1028; 00.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS: Bhattramakki, Dinakar
AUTHORS: Blthon, Thomas E.
TITE: Heat-Stress Response of Maize Mitochondria
JOURNAL: Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.1%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches
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ION: (1)..(1028)
INFORMATION: Zea Mays L., Line B73
                                                                                                                                                                                                                                                                                                                                                                                                          ON: (424)..(693)
INFORMATION: Heat Shock Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-198-119C-56/c; Sequence 56, Application US/09198119C; Patent No. 6417428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 ATACTGATAGAAGATAGA 863
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APPLICANT: Thomashow, Michael
APPLICANT: Stockinger, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: S'UTR
LOCATION: (1)..(78)
PUBLICATION INFORMATION:
AUTHORS: LUNG, Adrian A.
AUTHORS: Blum, Paul H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AME/KEY: transit peptide
GOCATION: (79)..(213)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poly A site (1028) ... (1028)
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(329)..(1028)
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LOCATION: (736)..(1028)
                                                                                                                                                                                                                                                                                                                                                                                 NAMB/KBY: misc feature
LOCATION: (424)..(693)
                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: (79)..(735)
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LOCATION: (1)..(1028)
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OCATION: (1)..(1163)
THER INFORMATION: Zea Mays L., Line B73
                                                                                                                                        AME/KEY: misc feature
OCATION: (559)..(828)
THER INFORMATION: Heat Shock Domain
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Patent No. 6562958
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-2704
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(79)..(213)
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(1163)..(1163)
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; LOCATION: (871)..(1163)
US-09-249-180-5
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(329)..(463)
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(447)..(1163)
                                                   (1)..(1163)
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Matches 18; Conserv
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LOCATION: (1)..(78)
FEATURE:
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US-08-545-528D-1
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APPLICANT: Dund, Adrian A
APPLICANT: Dund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Blattramakki, Dinakar
APPLICANT: Rhoads, David M.
TITLE OF INVENTION: Isolation and Characterization of Heat Shock Protein
FILE REPERENCE: UNVN52819
CURRENT APPLICATION WUMBER: US/09/249,180
CURRENT FILING DATE: 1999-02-12
EARLIER APPLICATION WUMBER: 60/076/014
EARLIER APPLICATION NUMBER: 60/076/014
EARLIER OF SEQ ID NOS: 7
SOFTWARE: Created in Patentin Ver. 2.0, Edited in WordPerfect 6.1
                     DB 4; Length 1132; 27;
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ilarity 100.0%; Pred. No. 27,
Conservative 0, Mismatches
                                                                                                                                          PRIOR PELICATION NUMBER: US 08/706,270
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR APPLICATION NUMBER: US 09/018,227
                                                                                                                                                                                                                                                                                                            MBER: US 09/018,227
1998-02-03
                                                                                                                                                                                                                                                                                                                                                    PRIOR FILLING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,234
PRIOR FILING DATE: 1998-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-09-249-180-5/c
Sequence 5. Application US/09249180
Patent No. 6268548
GENERAL INFORMATION:
 Kirsten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver.
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Best Local Similarity
Matches 18; Conserva
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ORGANISM: Zea mays
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LOCATION:
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ABPLICANT GATY L. Breton et.al.

APPLICANT GATY L. Breton et.al.

APPLICANT GATY L. Breton et.al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GT-0599-0378

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 2704

LENGTH: 2148
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Length 1163;
                                                       0; Indels
  DB 3;
     Query Match 1.1%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 27, Matches 18; Conservative 0; Mismatches
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Gaps

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APPLICANT: KERNE, JACK D.
APPLICANT: KERNE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
APPLICANT: LEVING, PETER H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: NOTOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE DREFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
CHARTH: 4411529
TYPE: DNA
CRGANISM: Mycobacterium tuberculosis
COTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 4411529;
20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WHERE: US/08/120,827
FILING DATE: 15-SEP-1993
CLASSIFICATION: 435
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100.0%; Pred. No. -...
0; Mismatches
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100.0%; Pred. No.
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Patent No. 5525495
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NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELEGIONARY TO TELECOMMUNICATION: TELECOMMUNICATION: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703) 413-2220
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Best Local Similarity 100.
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STATE: Virginia
COUNTRY: U.S.A.
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Best Local Similarity
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STREET: 17
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                                                                                         GENERAL INCRMATION:
APPLICANT: Fraser et al.
APPLICANT: Fraser et al.
PUTILE OF INVENTION: Nuclectide Sequence of the Mycoplasma Genitalium Genome, Fragment Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REPERENCE: PB193P1
CURRENT FILING DATE: 1995-10-19
PRIOR PILING DATE: 1995-66-07
PRIOR FILING DATE: 1995-66-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Version 3.1
SEQ ID NO. 1
LENGTH: 580073
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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1.1%; Score 18; DB
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches
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Patent No. 6294328
                                                     Sequence 1, Application US/08545528D
Patent No. 6537773
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ORGANISM: Mycoplasma genitalium
JS-08-545-528D-1
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JS-09-103-840A-2/c
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Length 210;

DB 4;

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-00-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 2, 2004, 07:59:13 Job time: 134.678 secs
                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 17; Best Local Similarity 100.0%; Pred. No. Matches 17; Conservative 0; Mismatci
                                                                                                                                                                                                                                                ; TYPE: DNA; Caphylococcus epidermidis
US-09-134-001C-2588
                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 AAACAAGCATCATTAAA 237
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APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE-Stamm et al
APPLICANT: LYND DOUGETE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                  Sequence 71, Application US/08478675

Patent No. 5773246

GENERAL INFORMATION:
APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
GITY: Alington
STATE: Virginia
COUNTRY: U.S.A.
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1.0%; Score 17; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 0; Indels
  Indels
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MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
STILING DATE: 0'--UWN 1996
CLASSIFICATION NUMBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INPORMATION:
NAME: Oblon, No. 5773246man F.
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
TELECOMMUNICATION NUMBER: 714-158-0 CIP
  ;
0
0; Mismatches
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; Sequence 2588, Application US/09134001C
; Patent No. 6380370
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                                              1315 AACAATAAAAGAAAAAC 1331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)413-2220
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unkn
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  17;
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Sequence 3729, Ap Sequence 3729, Ap Sequence 54, Appl Sequence 707, Appl Sequence 1633, Ap Sequence 3, Appli Sequence 54726, A Sequence 294129, Sequence 294129, Sequence 14103, Ap Sequence 18166, A Sequence 18166, A Sequence 18166, A
                                                                                                                                      2, 2004, 03:00:32 ; Search time 1254.7 Seconds (without alignments) 4871.226 Million cell updates/sec
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                                                                                                                                                                                                                                                                                            ggttaagcgttttacttatg.......tttctctctagctatatttta 1677
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cgn2_6/ptodata1/pubpa/PCT_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO6_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO6_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO6_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO8_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO9_PUBCOMB.seq:*

cgn2_6/ptodata1/pubpa/USO9_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO9_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO9_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO9_NEW_PUB.seq:*

cgn2_6/ptodata1/pubpa/USO8_NEW_PUB.seq:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-938-842A-3729
US-09-930-213-54
US-09-803-719-707
US-09-803-719-707
US-09-803-719-706
US-10-191-807-3
US-10-027-632-54726
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Maximum DB seq length: 200000000
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Match Length DB
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38998 88862, App 88862, App 88862, Ap 88862, Ap 88863, Ap 230239, Ap 230239, Ap 1330239,	133067, 34038, A 3975, Ap 262153, Ap 262153, 262153,	nce 262154, nce 122375, nce 122375, nce 30495, A nce 30496, A nce 30496, A nce 30496, A nce 30496, A nce 30496, A	Service Control to the Control of th	1 420 200 600	Gaps 0.
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		2621154 11223375 1223375 132496 132496 1333 1333 1333 1322 1333	Outre 1		DB 10; Len
US-08-781-986A,3898 US-10-029-386-39886 3 US-10-027-632-88862 4 US-10-027-632-88862 4 US-10-027-632-88863 5 US-10-027-632-88863 5 US-10-027-632-230239 4 US-10-027-632-230239 5 US-10-027-632-230239 6 US-10-027-632-230239 6 US-10-027-632-230239 6 US-10-027-632-230239 6 US-10-027-632-230239	138-10-027-632 138-10-027-632 1-03-10-027-632 1-03-10-027-632 1-03-10-027-632 138-10-027-632	13-10-027-632 13-10-027-632 13-10-027-632 13-10-027-632 13-10-027-632 13-10-027-632 13-09-938-842 13-09-938-842	LIGNMEN 342A	SAMES AND METHODS OF USE 1130-3 AND METHODS	Score 1677; Pred No. 0; 0; Mismatches
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00 00	ପ୍ରପ୍ରପ୍ର ପ୍ରପ୍ରପ୍ରପ୍ର		RESULY US-09- 1 Sequ 1 Pate 1 APP 1 APP 1 APP	HEDDRARGAR BOU	US-09 US-09 Que Best

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GGTTAAGCGTTTTTACTTATAGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 60 TITITCAGATCATCAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120

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OY 1201 AAAGCTACGTATTCATTGGGAGTGTACTAGTAACTAGTAACTACCAACAATGACT 1280 Db 1201 AAAGCTAGGTATTTCATTTGGGAGTGTACTAACTACTAACTA	0y 1381 TCCCATAATAATACTGATAGAAGATAGAAAGGAAAGGAA	SULT, 2 -09-938 -09-938	GENERAL INFORMATION: APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel APPLICANT: Kreps, Joel APPLICANT: Kreps, Joel APPLICANT: Zhu, Tong TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONT TITLE OF INVENTION: SAME, AND WETHODS OF USE FILLE REFERENCE: SCRIP1300-3 CURRENT PELLING DATE: 2001-08-24 CURRENT PLING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR PELLON DATE: 2000-08-24 PRIOR APPLICATION NUMBER: US 60/264.647	APPLIANG DATE: 2001-01-16 APPLICATION NUMBER: US 60/300,111 R OF SEQ ID NOS: 5379-6-22 NO 3729 HT. 1677 NISM: Arabidopsis thaliana NISM: Arabidopsis thaliana 8-8424-3729 Match	Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gape 0. Oy 107TAAGCOTTTTATATATATATATATATATATATATATATATATAT
121 GARATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGTGTTATCTGAAGAGA		481 AAGCCTAAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTCTAATTCTAATCCC 540 481 AAGCCTAAAAGGTTACTACCGGTTTGACGGTTTATAATTTCTAATCCC 540 481 AAGCCTAAAAGGTTACTACCGGTTTATAATTTGGTGTTTAATTCTAATCCC 540 541 GGATCCGTTTGTTTGTTATTTGTTAATCTCAAGCCACGTTATCGCCAATATTTTTGAGTG 600 541 GGATCCGTTTGTTAGTTAATCTCAAAGCCACGTTATCGCCAATATTTTTGAGTG 600 601 GGTAGCGAATGGTGGAGTCGAATAGTTGGGCCTCAACAATGTTGTGGAACTGAAG 660 601 GGTAGCGAATGGTGGAGTCGAATAGTTGGGCCTCAACAATGTTGTGGAACTGAAG 660 601 GGTAGCGAATGGTGGAGTCGAATAGTTGGGCCTTAACAATGTTGTGGAACTGAAG 660 601 GGTAGCGAATGGTCGAATAGTTGGGCCTTAACAAATGTTGTGGAACTGAAG 660	661 AGAGTAGGGTCCAGCTCAGGCCCACATTCCATTTGTAGCCTTTCTTT	AACTIACAATCAITTCGAITACTITGAICCTGATTTCTAGTTCGGTTTGTTGTTTATTTTTTTTTT	1021 ATTGARATCTTTTCCAACCTTATAAAGTTAATTGCCTAACCCCAAGTATG 1080 1081 GGCTTACAGCTTTTTCCATAAAATTTAAAGTTAATTGCCTAACCCCAAGTATG 1080 1081 GGCTTACAGCTTTTTCCATAAAATTTAAAGTAAATCTTTTTTTCCTAACCAATAAAAATT 1140 1081 GGCTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTCCTAACCAATAAAAATT 1140 1141 ATTGAAAATCTTTCCAACCATAGAAAATTAAATTTGATCAGGGATGGAAATTTTTGTAC 1200 1141 ATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTAC 1200 1141 ATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTAC 1200

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	601 GGTAGGGAATGGTGGGGTTCGAATAGTTGGGCCTCAACAATGTGTGGGAACTGAAG 601 GGTAGGGAATGGTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG 601 GGTAGGGAATGGTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG 601 GGTAGGGATCCAGCTCCAGTCCAATTGTTTGTTTTTTTTT	1141 ATTGARARTTTTCCARCCATRGARAGTTAARTTTGATCRGCGATGGARATTTTTGTAC 1200 1141 ATTGARARTCTTTCCARCCATGARARGTTAARTTTGATCGCGATGGARATTTTGTAC 1200 1201 AARGCTAGGATTTGGGAGTGTAACTTAATTTGATCCATACAACGAAAGTTTTTGTAC 1200

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APPLICANT: ROSENTHAL, ANDRE
APPLICANT: HINZMANN, BERND
APPLICANT: CHARFER, RZINHARD
APPLICANT: CHARFER, CHARNES
APPLICANT: TCHE-NITSE, OLEG
APPLICANT: TCHE-NITSE, OLEG
APPLICANT: GRIES, MARTIN
APPLICANT: GRIES, MARTIN
APPLICANT: GRIES, MARTIN
APPLICANT: SERS, CHRISTINE
TILLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
FILE REFERENCE: ALBRE-14
CURRENT APPLICATION NUMBER: US/09/930,213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                               APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TILLE OF INVENTION: Human Genes and Gene Producte
FILE REFRENCE: 1624.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.3%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 7.3
Matches 21; Conservative 0; Mismatches
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PRIOR FILING DATE: 2000-01-31
NUMBER OF SRQ ID NOS: 885
SOFTWARE PatentIn Ver. 2.1
SEQ ID NO 306
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 306, Application US/09930213
Publication No. US20030170625A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 TTATCCCTCTGTGGTGGACCC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 TTATCCCTCTGTGGTGGACCC 436
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ORGANISM: Homo sapiens
US-09-930-213-306
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-1633
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US-09-930-213-306
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APPLICANT: Labat, Ivan
APPLICANT: Kita, David
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1644.002
FILE REFERENCE: 1644.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                  GENERAL INCORPATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Berobedo, Jaime
APPLICANT: Berobedo, Jaime
APPLICANT: Brochedo, Jaime
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Reinhard, Christoph
APPLICANT: Rendazzo, Filippo
APPLICANT: Rendazzo, Filippo
APPLICANT: Kennedy, Giulia C.
APPLICANT: Kennedy, Giulia C.
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Lamson, George
APPLICANT: Crkvenjakov, Radomir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Giese, Klaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1633, Application US/09803719
Publication No. US20030044783A1
148 TTATCCCTCTGTGGTGGACCC 168
                                                                                                                      Application US/09803719
5. US20030044783A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 TIAICCCICIGIGGACCC 436
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100.0%; Pre
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rmanac, Snezana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-803-719-707
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Best Local Similarity
Matches 21; Conserv
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q à

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TITLE OF INVENTION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-04-30

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-36

PRIOR FILING DATE: 1999-11-36

PRIOR PILING DATE: 1999-11-36

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-10-38

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-38

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 294129

LENGTH: 627
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100.0%; Pred. No. 2...
0; Mismatches
                                                                             Sequence 294129, Application US/10027632
Publication No. US20030204075A9
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) COATTON: (1)...(627)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO1275-PROY
CURRENT APPLICATION NUMBER: US/10/191,807
CURRENT FILING DATE: 2002-07-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US, 10/0/27, 632
CURRENT APPLICATION NUMBER: US, 60/18, 066
PRIOR APPLICATION NUMBER: US, 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US, 60/16, 363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-108-28
PRIOR FILING DATE: 1999-108-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54726
LENGTH: 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.3%; Score 21; DB 15; Length 108359;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 20; DB 13; Length 627; llarity 100.0%; Pred. No. 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -10-027-632-54726/c
Sequence 54726, Application US/10027632
Publication No. US20030204075A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 TIAAAIGGITIGIAAGAAIA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(108359)
; OTHER INFORMATION: n = A,T,C or G
JS-10-191-807-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(627)
OTHER INFORMATION: n = A,T,C or G
JS-10-027-632-54726
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 108359
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DB 13; Length 627; 25; 0; Indels

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PRINGAL INFORMATION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide FITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,006

PRIOR PILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

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PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                           Sequence 54726, Application US/10027632
1134 AAAAATTATTGAAAATCTTT 1153
                                                                              508 AAAATTATTGAAATCTTT 489
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508 AAAAATTATTGAAAATCTTT 489

us-09-938-842a-3729.oli.rnpb

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SEQ ID NO 9987
LENGTH: 768
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ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PAPPLICATION NUMBER: US/10/027,632
CURRENT PAPPLICATION NUMBER: US/02.04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1999-11-3
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-3
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR PILING DATE: 1999-109-08-09
PRIOR PILING DATE: 1999-109-08-09
PRIOR PILING DATE: 1999-109-08-09
PRIOR PILING DATE: 1099-108-09-08-09
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.00.0%; Pred. No. 25;
.ve 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 294129, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 9987, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            1134 AAAATTATTGAAAATCTTT 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1134 AAAAATTATTGAAAATCTTT 1153
                                                                                                                                                                                                                                                                                                                                                                                508 AAAATTATTGAAAATCTTT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508 AAAATTATTGAAAATCTTT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1) ... (627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
                                                                                                       ) LOCATION: (1)...(627)
) OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54726
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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1.2%; So
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
                                                                             NAME/KEY: misc_feature
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US-09-815-242-9987/c
TYPE: DNA
ORGANISM: Human
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Sequence 14103, Application US/10029386
Publication No. US20030194704A1
GABREAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hank, David R.
APPLICANT: Hank, David R.
TITLE OF INVENTION: HUMAN GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
TITLE OF INVENTION: HUMAN GRNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
TITLE OF INVENTION: AFONICA.X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N: MAP TO AL135926.3

N: EXPRESSED IN HEALT, SIGNAL = 1.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 1.1

N: EXPRESSED IN HELA, SIGNAL = 1.1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

N: EXPRESSED IN LIVER, SIGNAL = 1.6

N: EXPRESSED IN LIVER, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2

N: EXPRESSED IN LIVE, SIGNAL = 1.2
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TITLE OF INVEXTION:
TITLE OF INVEXTION:
TITLE OF INVEXTION: Identification of Essential Genes in
TITLE OF INVEXTION: Identification of Essential Genes in
TITLE OF INVEXTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 06/191,078
PRIOR PELING DATE: 2001-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/25/931
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FREESED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9; Length 768;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14103
LENGTH: 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1249 ACCAGAATGAGTT
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-9987
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GENERAL INFORMATION:

Patent No. US20020131160A1

GENERAL INFORMATION:

PAPELICANT: Warren, Wesley C.

APPLICANT: Byatt, John C.

APPLICANT: Byatt, John C.

APPLICANT: Mariangan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 37-21 (10297) C.

FILE REFERENCE: 37-21 (10297) C.

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: US 09/465,231

PRIOR APPLICATION NUMBER: US 60/113,678

PRIOR FILING DATE: 1998-12-15

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANI: Litew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPERENCE: 4231/2005
FILE REPERENCE: 4231/2005
CURRENT FILING DATE: 2002-09-12
FRIOR APPLICATION NUMBER: US 10/085, 783
FRIOR APPLICATION NUMBER: US 60/305, 340
FRIOR FILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 60/275, 017
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-03-12
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Pred. No. 76;
    Length 199;
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DB 13;
73;
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100.0%; Pred. No. ...
Query Match 1.1%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 73; Best Local Similarity 100.0%; Prede 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18166, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
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LoCATION: (31)
OTHER INFORMATION: n is a, c, g, or t
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Human
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